

Stochastic Model Results
Bifurcation Results
Design 1

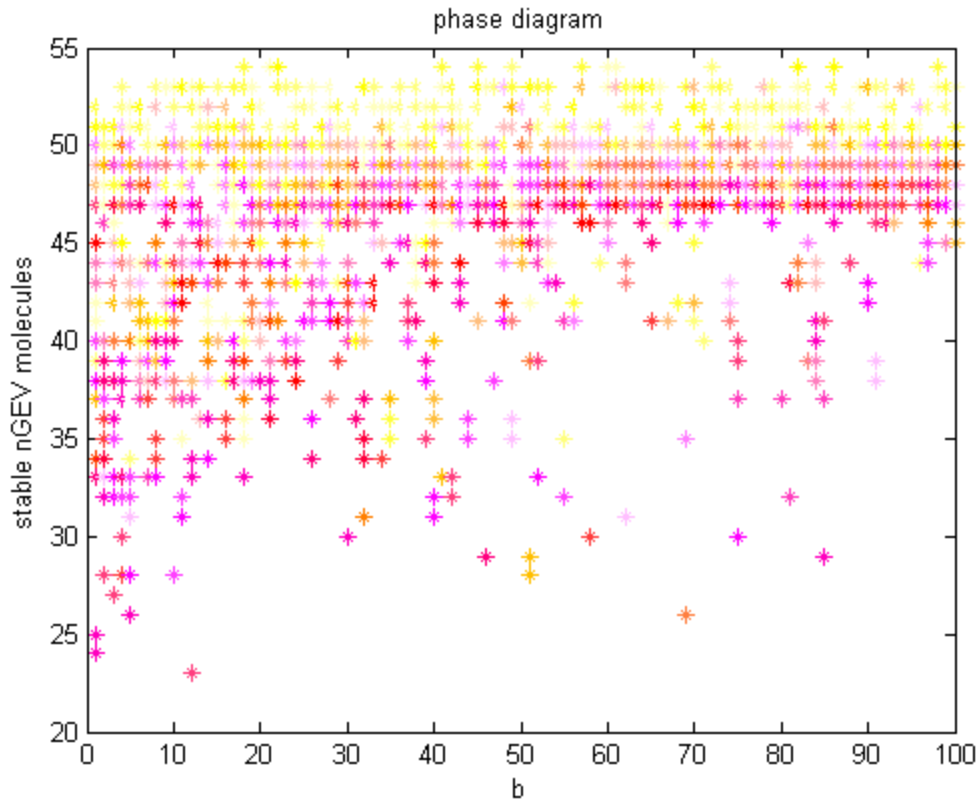


Figure 1. Results of a Bifurcation analysis of the basal rate constant(b) of the expression of GEV and rrtTa genes. Plot shows the effect varying basal rate has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of b studied. The values of b studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

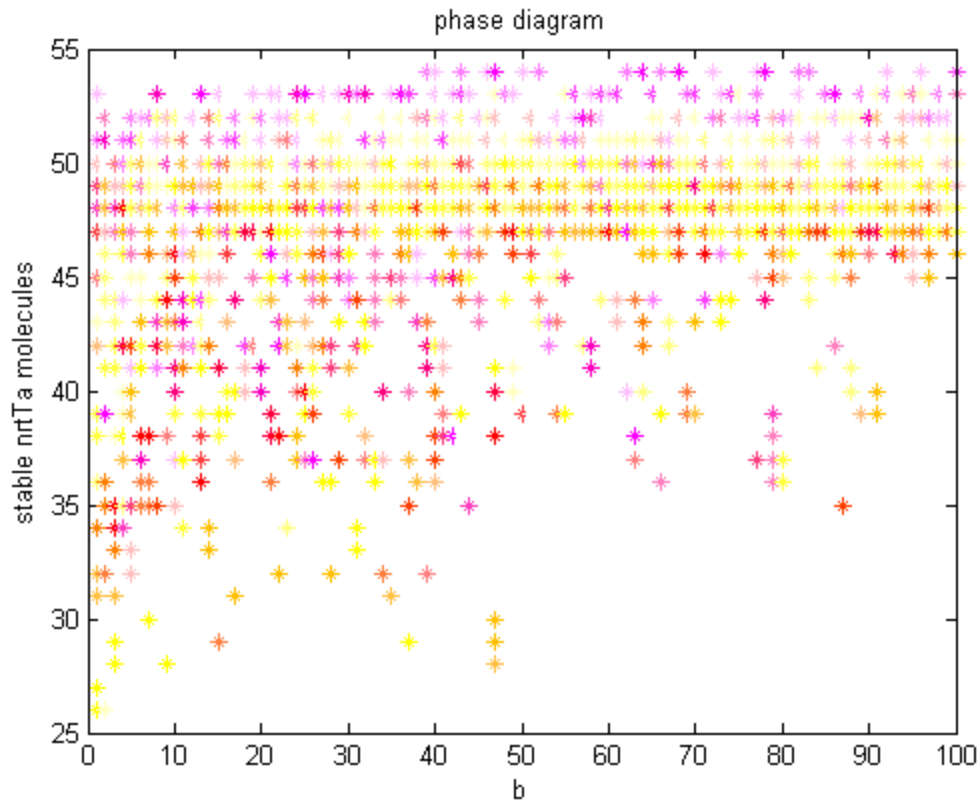


Figure 2. Results of a Bifurcation analysis of the basal rate constant(b) of the expression of GEV and rT α genes. Plot shows the effect varying basal rate has on nrt α levels. Expression of rT α is measured by the amount of nrt α found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrt α molecule populations ranging between 0 and 4) for each value of b studied. The values of b studied were the 100 integers between 0 and 100. The populations of nrt α at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrt α molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

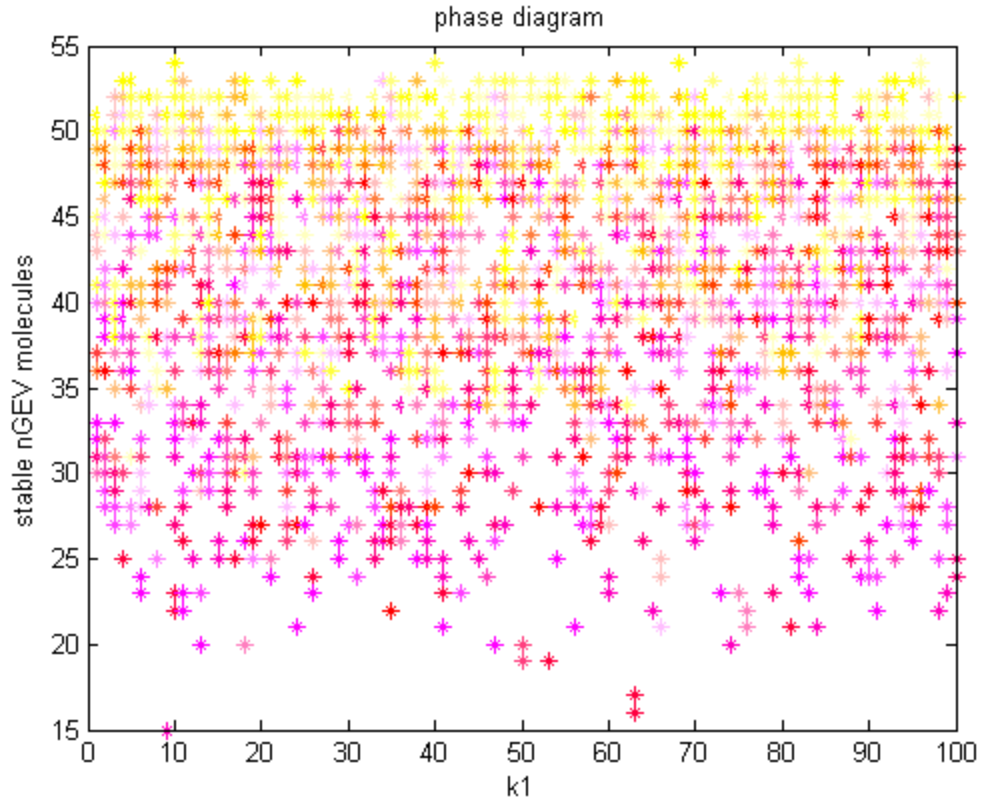


Figure 3. Results of a Bifurcation analysis of the Binding Rate constant(k_1) of GEV and rTta to their respective binding sites. Plot shows the effect varying k_1 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_1 studied. The values of k_1 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

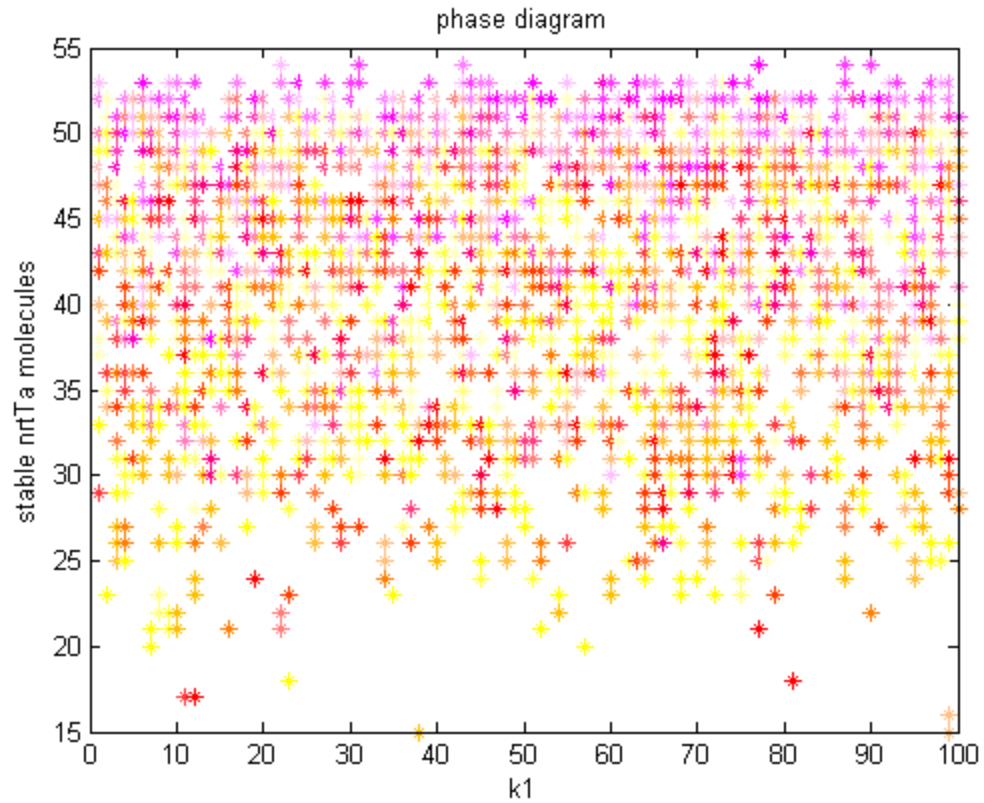


Figure 4. Results of a Bifurcation analysis of the Binding Rate constant(k_1) of GEV and rT_a to their respective binding sites. Plot shows the effect varying k_1 has on nrtT_a levels. Expression of rT_a is measured by the amount of nrtT_a found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtT_a molecule populations ranging between 0 and 4) for each value of k_1 studied. The values of k_1 studied were the 100 integers between 0 and 100. The populations of nrtT_a at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtT_a molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

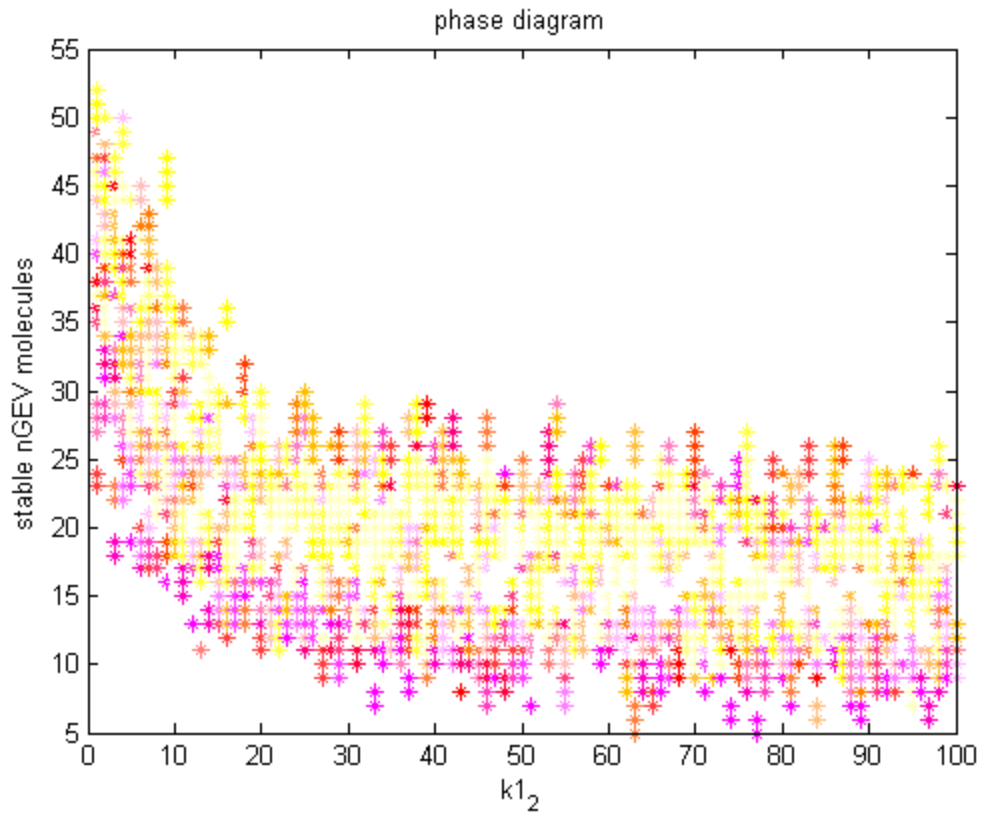


Figure 5. Results of a Bifurcation analysis of the Dissociation Rate constant(k_{1_2}) of GEV and rtTa from their respective binding sites. Plot shows the effect varying k_{1_2} has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_{1_2} studied. The values of k_{1_2} studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

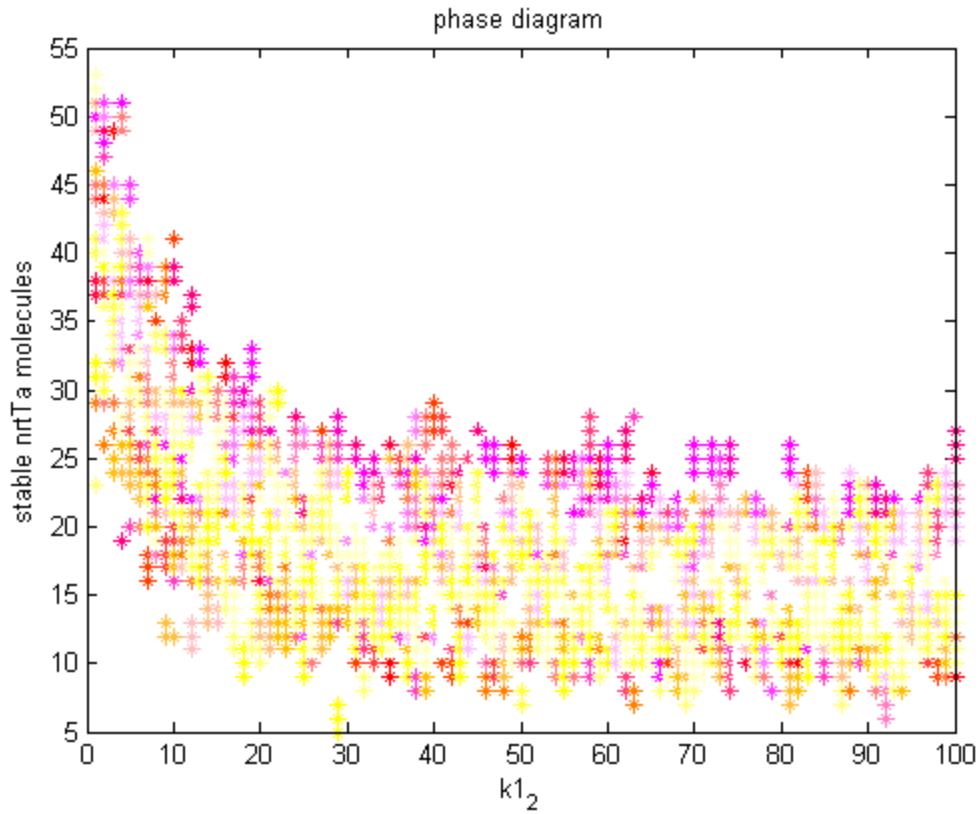


Figure 6. Results of a Bifurcation analysis of the Dissociation Rate constant(k_{1_2}) of GEV and rrtTa from their respective binding sites. Plot shows the effect varying k_{1_2} has on nrtTa levels. Expression of rrtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_{1_2} studied. The values of k_{1_2} were the 100 integers between 0 and 100. The populations of nrtTa at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

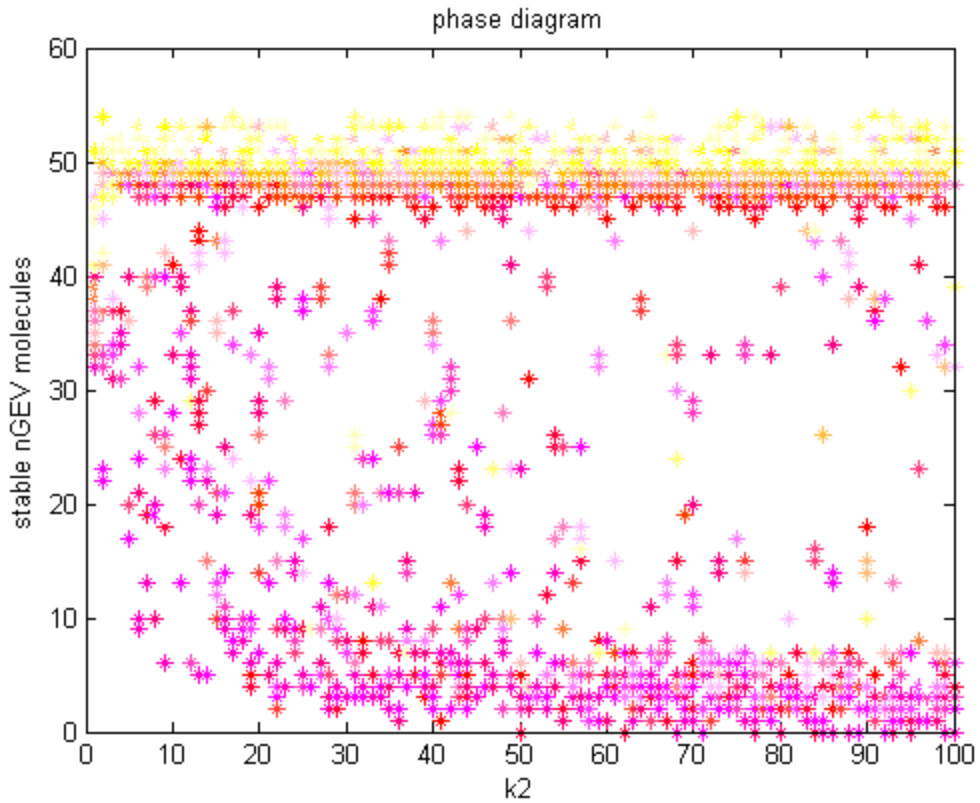


Figure 7. Results of a Bifurcation analysis of the Activated Transcription Rate constant(k_2) of the GEV and rtTa genes. Plot shows the effect varying k_2 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_2 studied. The values of k_2 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

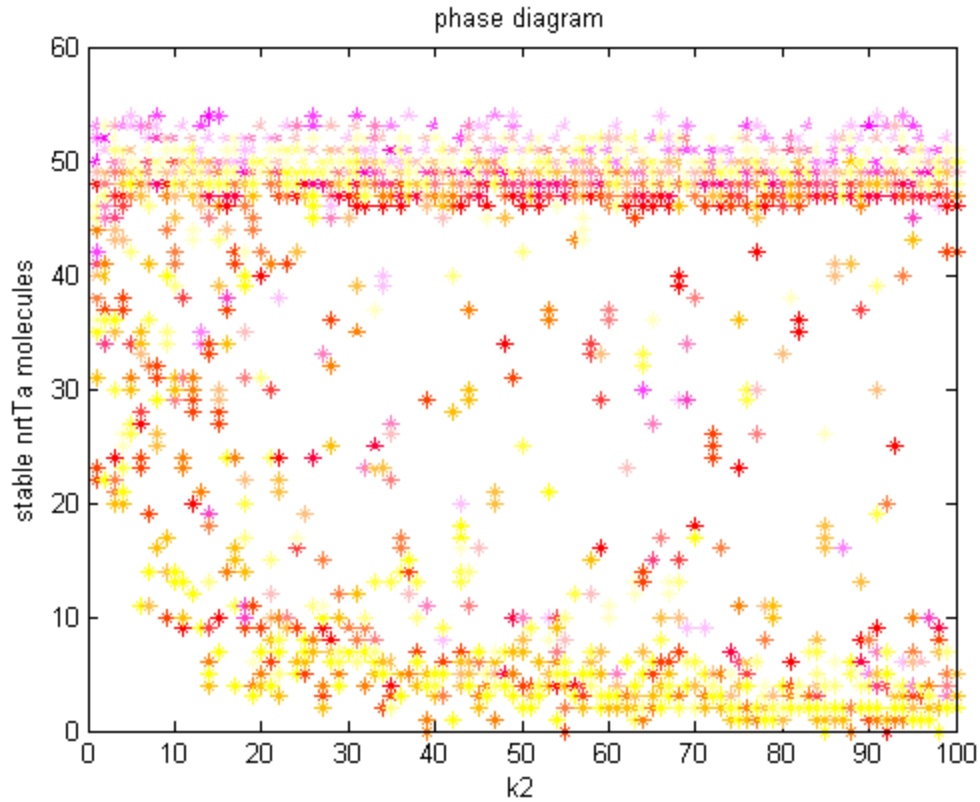


Figure 8. Results of a Bifurcation analysis of the Activated Transcription Rate constant(k_2) of the GEV and rtTa genes. Plot shows the effect varying k_2 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_2 studied. The values of k_2 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

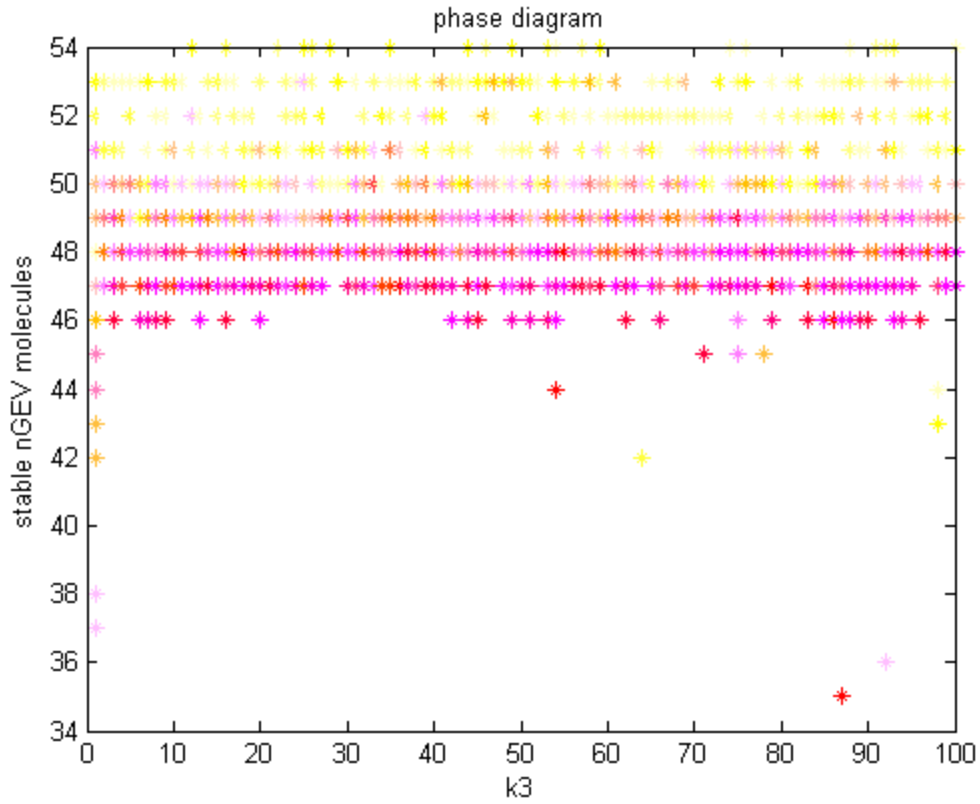


Figure 9. Results of a Bifurcation analysis of the Inhibited Transcription Rate constant(k_3) of the GEV and rtTa genes. Plot shows the effect varying k_3 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_3 studied. The values of k_3 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

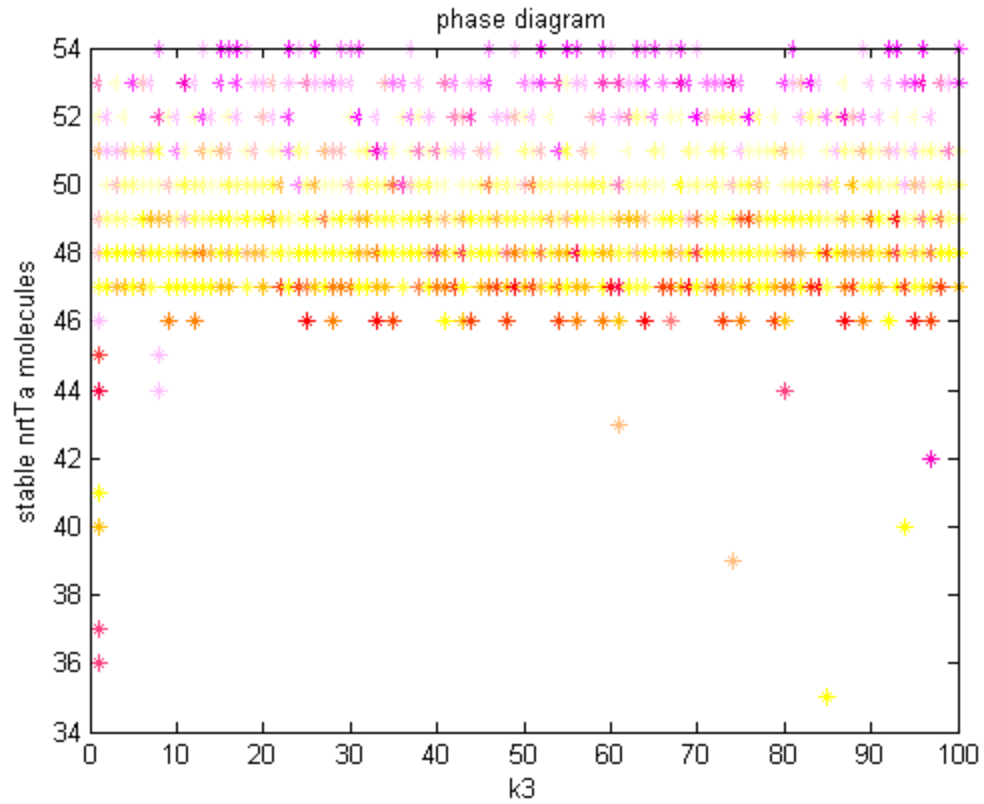


Figure 10. Results of a Bifurcation analysis of the Inhibited Transcription Rate constant(k_3) of the GEV and rtTa genes. Plot shows the effect varying k_3 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_3 studied. The values of k_3 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

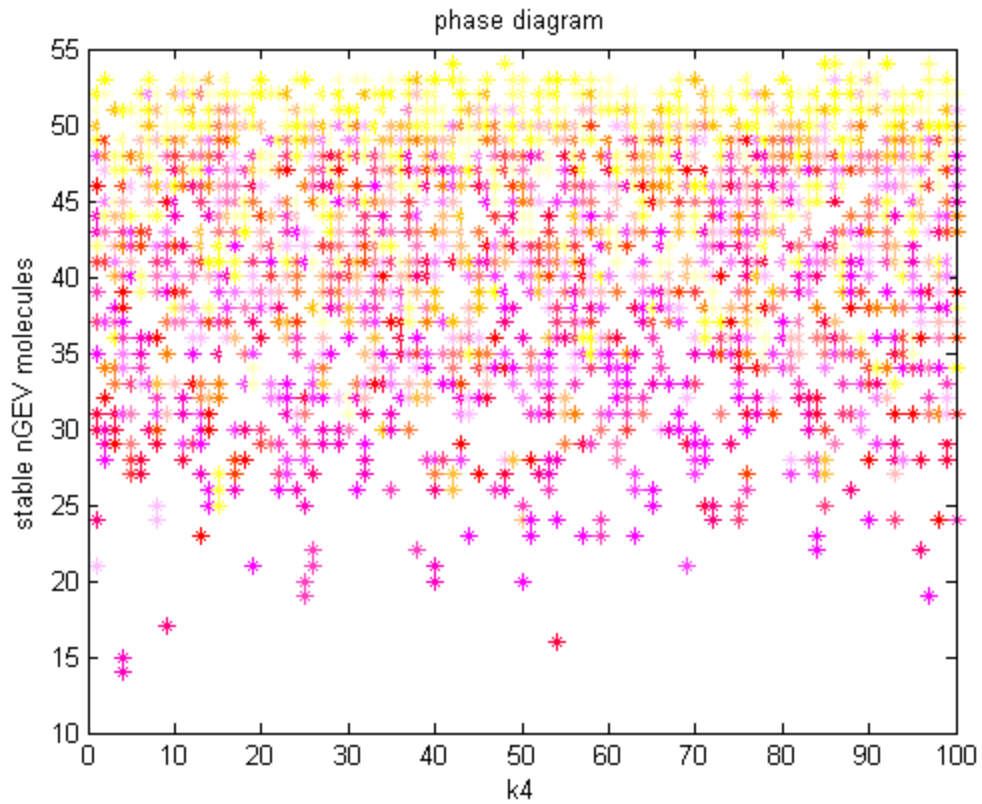


Figure 11. Results of a Bifurcation analysis of the Translation Rate constant(k_4) of the GEV and rrtTa mRNA. Plot shows the effect varying k_4 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_4 studied. The values of k_4 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

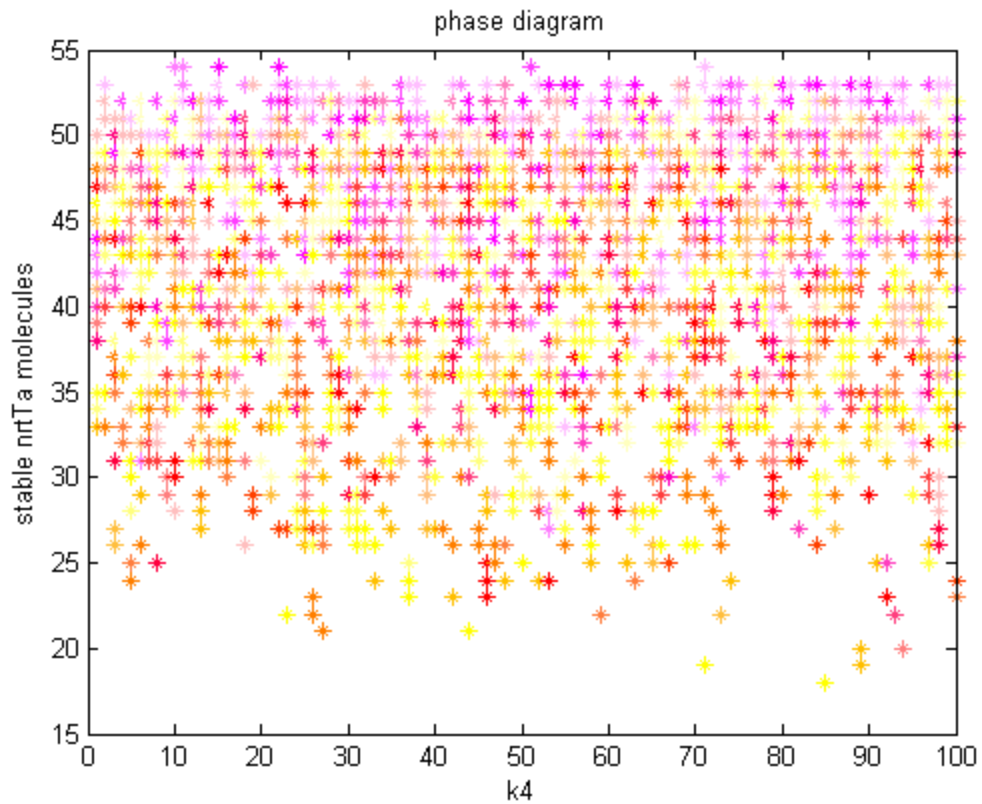


Figure 12. Results of a Bifurcation analysis of the Translation Rate constant(k_4) of the GEV and rtTa mRNA. Plot shows the effect varying k_4 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_4 studied. The values of k_4 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

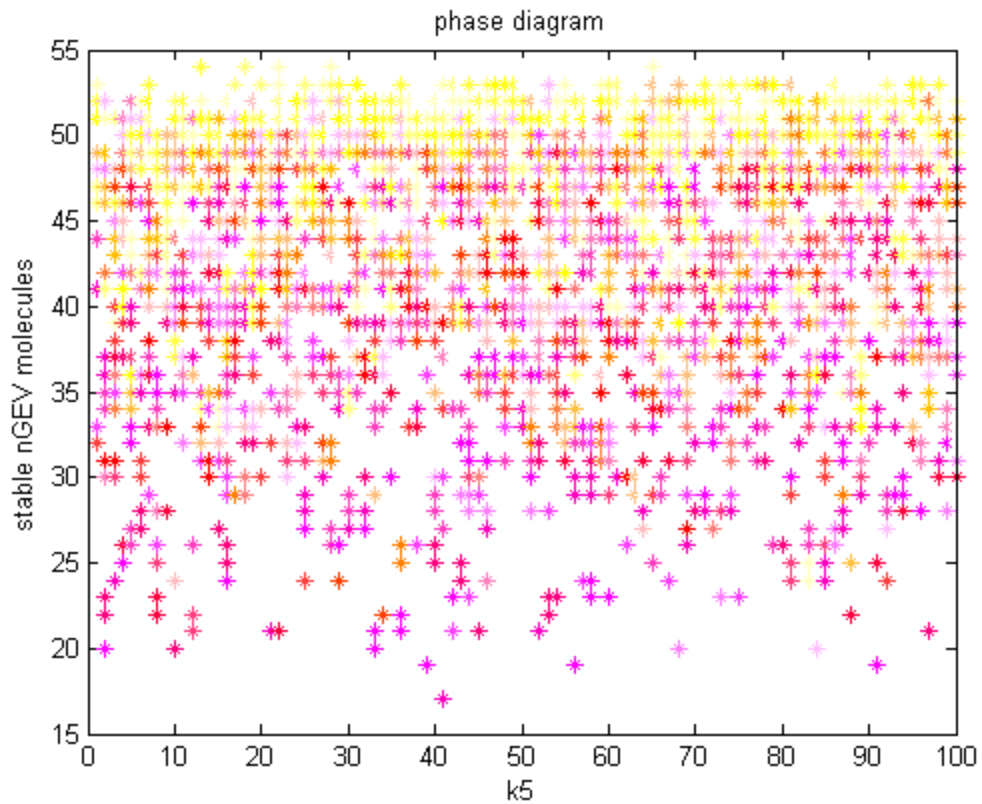


Figure 13. Results of a Bifurcation analysis of the Import Rate constant(k_5) of GEV and rTta from the cytosol to the nucleus. Plot shows the effect varying k_5 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_5 studied. The values of k_5 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

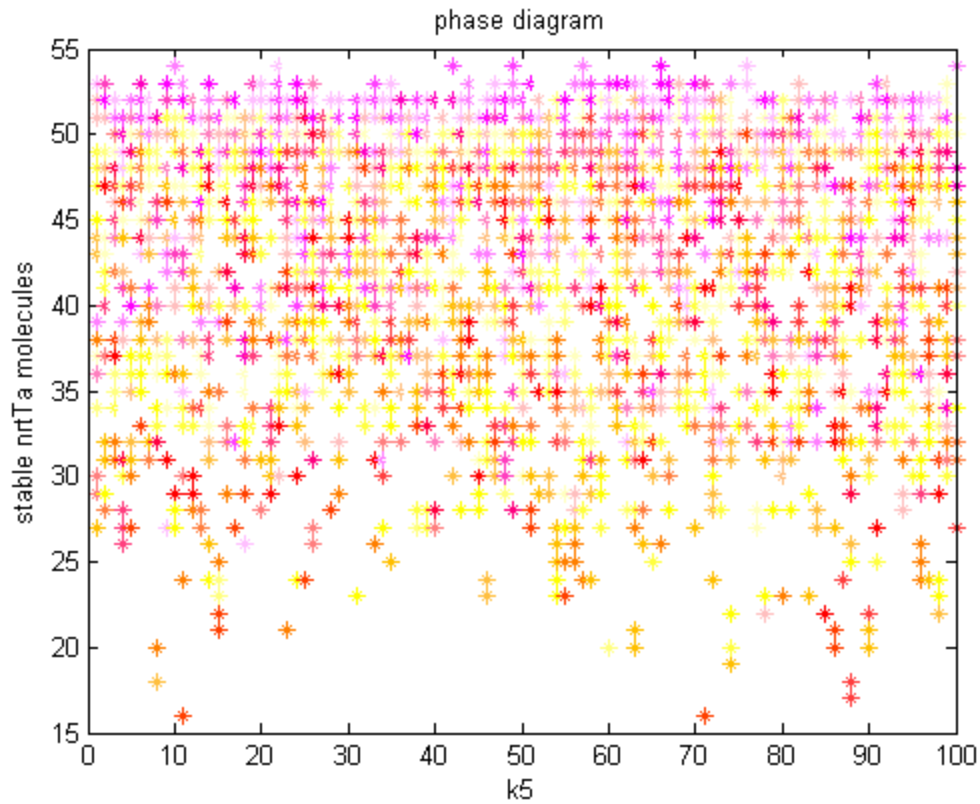


Figure 14. Results of a Bifurcation analysis of the Import Rate constant(k_5) of GEV and rT α from the cytosol to the nucleus. Plot shows the effect varying k_5 has on nrtTa levels. Expression of rT α is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_5 studied. The values of k_5 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

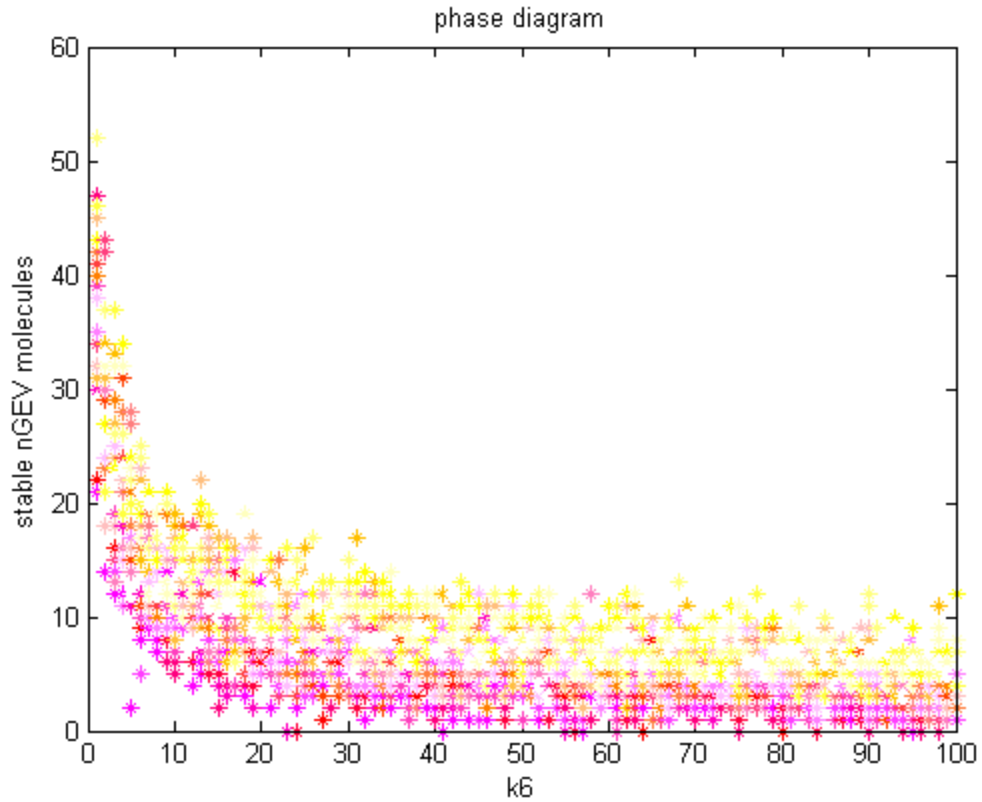


Figure 15. Results of a Bifurcation analysis of the Degradation Rate constant(k_6) of BFP and GFP. Plot shows the effect varying k_6 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_6 studied. The values of k_6 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

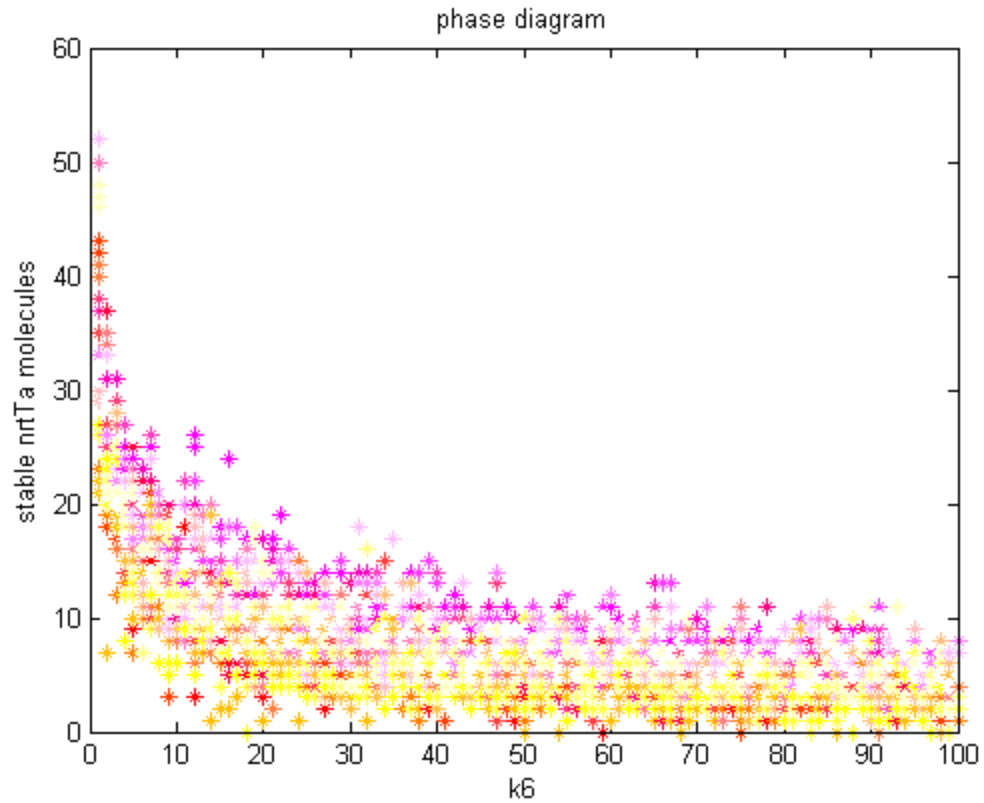


Figure 16. Results of a Bifurcation analysis of the Degradation Rate constant(k_6) of BFP and GFP. Plot shows the effect varying k_6 has on nrtTa levels. Expression of rT_a is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_6 studied. The values of k_6 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

Design 2

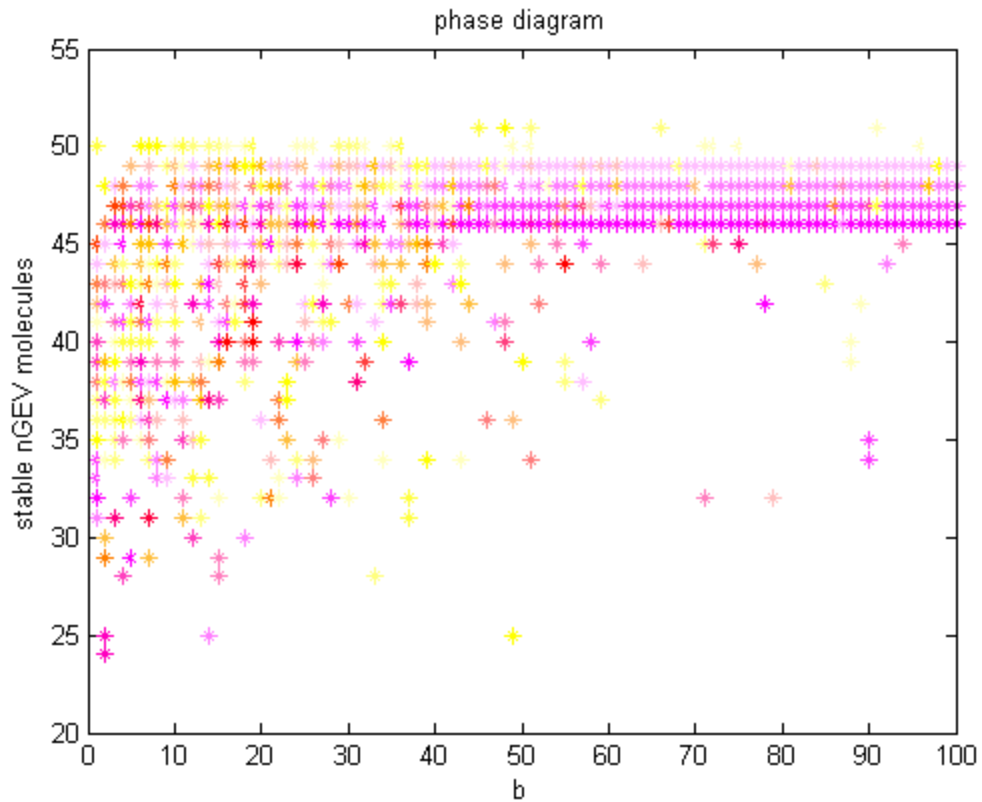


Figure 1. Results of a Bifurcation analysis of the basal rate constant(b) of the expression of GEV and rrtTa genes. Plot shows the effect varying basal rate has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of b studied. The values of b studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

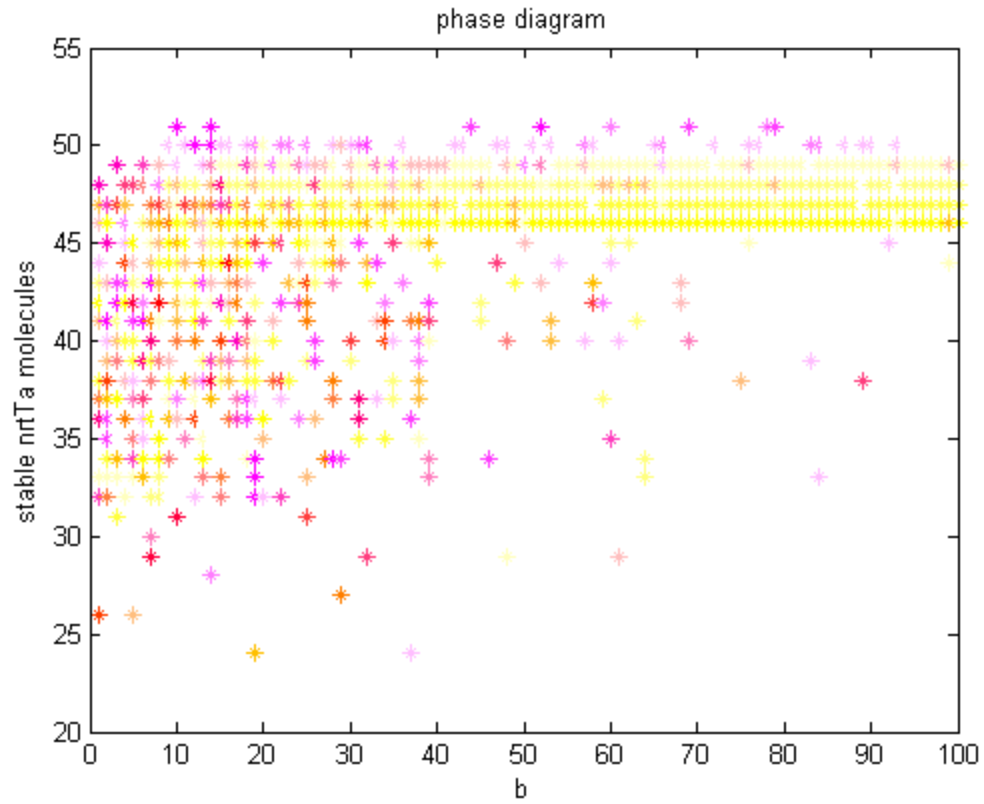


Figure 2. Results of a Bifurcation analysis of the basal rate constant(b) of the expression of GEV and rT_a genes. Plot shows the effect varying basal rate has on nrtTa levels. Expression of rT_a is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of b studied. The values of b studied were the 100 integers between 0 and 100. The populations of nrtTa at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

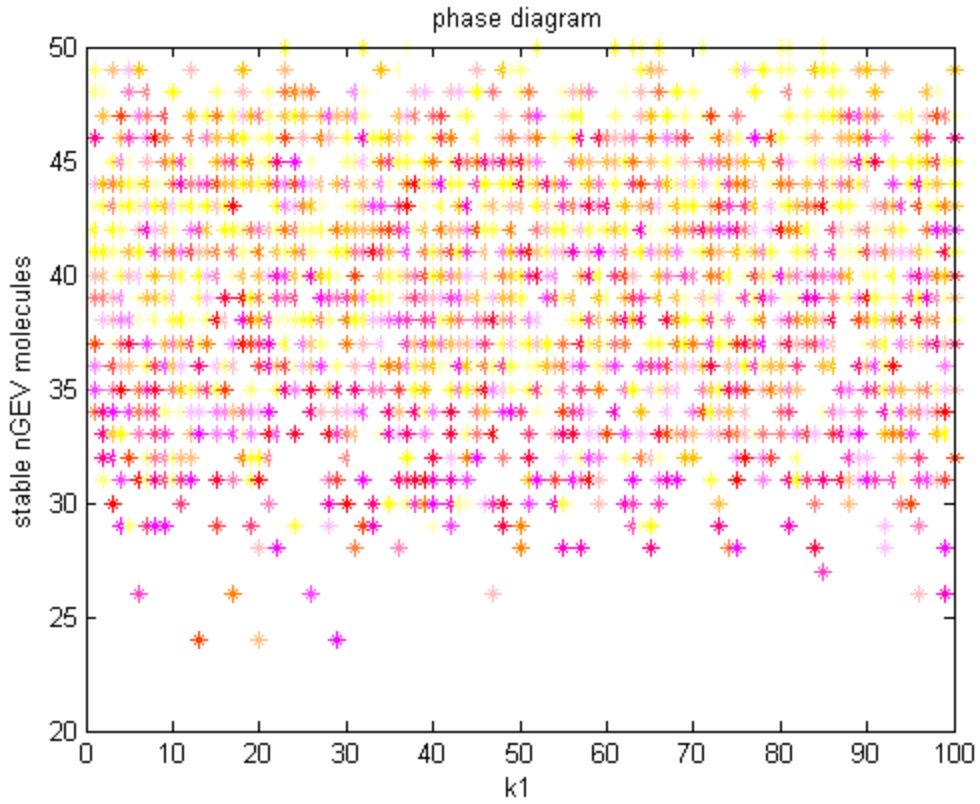


Figure 3. Results of a Bifurcation analysis of the Constitutive Binding Rate constant(k_1) of Lexa-vp16 to its binding sites. Plot shows the effect varying k_1 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_1 studied. The values of k_1 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

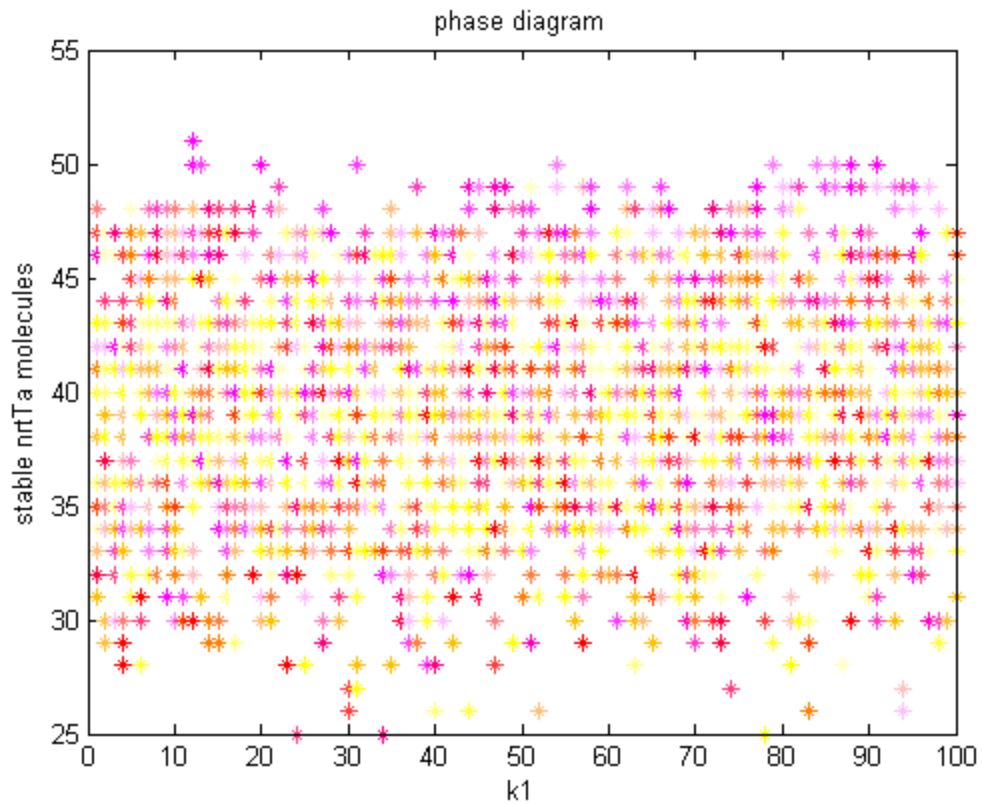


Figure 4. Results of a Bifurcation analysis of the Constitutive Binding Rate constant(k_1) of Lexa-vp16 to its binding sites. Plot shows the effect varying k_1 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_1 studied. The values of k_1 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

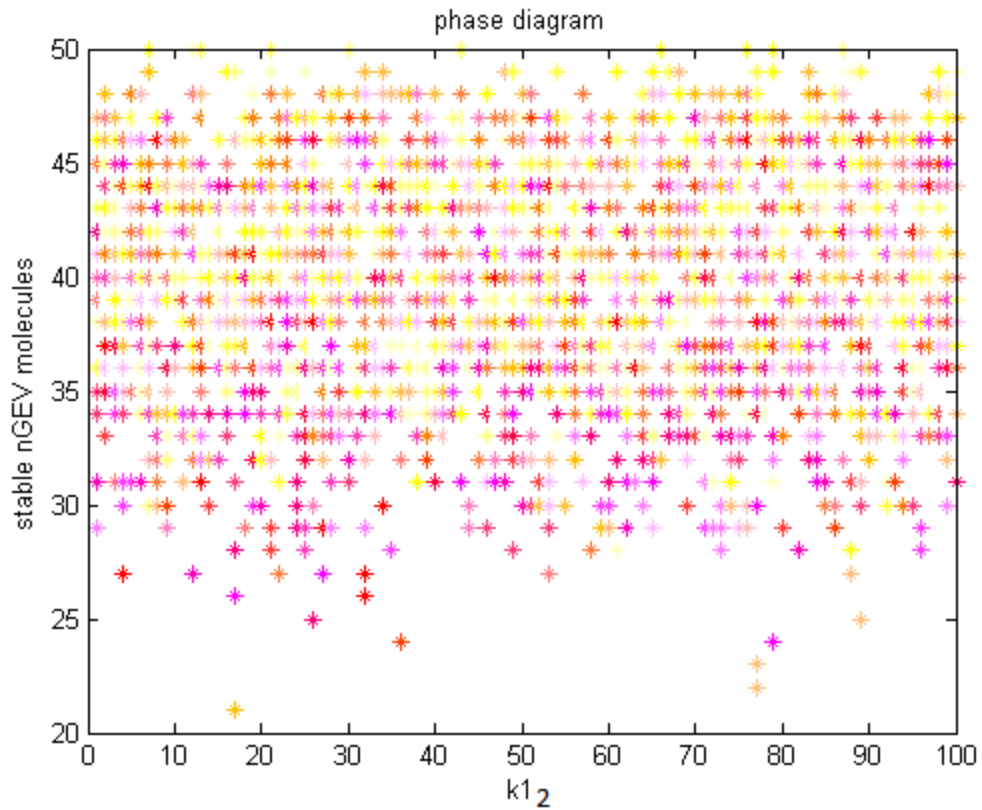


Figure 5. Results of a Bifurcation analysis of the Constitutive Dissociation Rate constant($k1_2$) of Lexa-vp16 from its binding sites. Plot shows the effect varying $k1_2$ has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of $k1_2$ studied. The values of $k1_2$ studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

Figure 6. Results of a Bifurcation analysis of the Constitutive Dissociation Rate constant(k_{1_2}) of Lexa-vp16 from its binding sites. Plot shows the effect varying k_{1_2} has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_{1_2} studied. The values of k_{1_2} studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

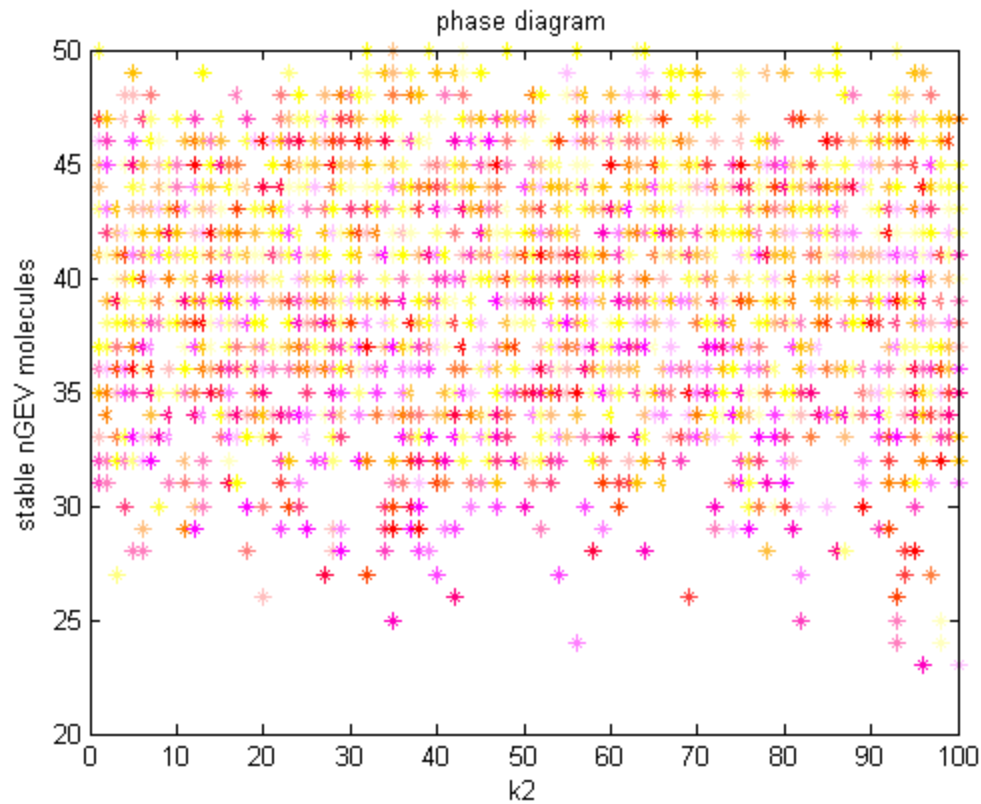


Figure 7. Results of a Bifurcation analysis of the Constitutive Transcription Rate constant(k_2) of the Constitutive GEV and rrtTa genes. Plot shows the effect varying k_2 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_2 studied. The values of k_2 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

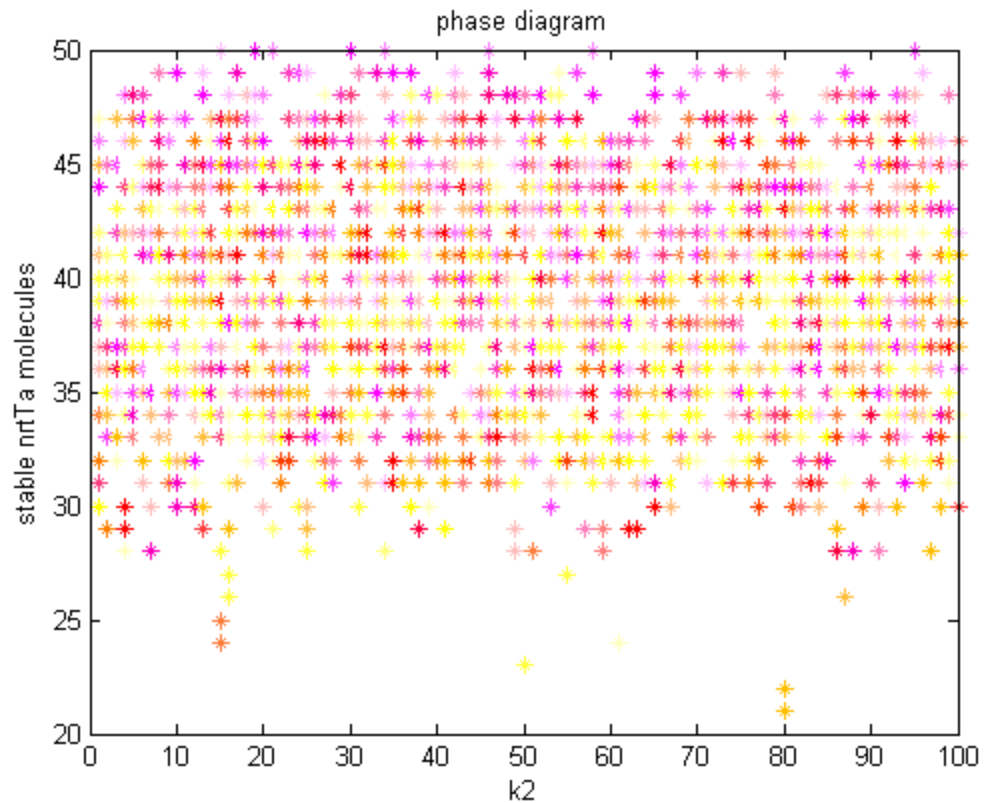


Figure 8. Results of a Bifurcation analysis of the Constitutive Transcription Rate constant(k_2) of the Constitutive GEV and rT_a genes. Plot shows the effect varying k_2 has on nrtTa levels. Expression of rT_a is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_2 studied. The values of k_2 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

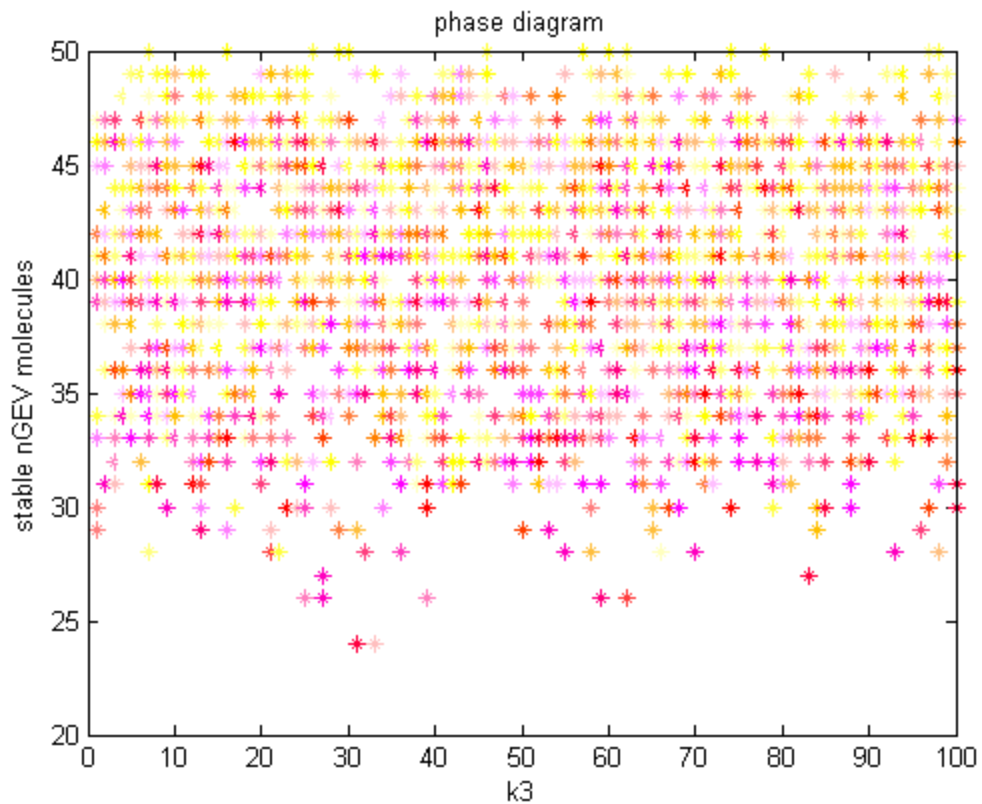


Figure 9. Results of a Bifurcation analysis of the Translation Rate constant(k_3) of the GEV and rtTa mRNA. Plot shows the effect varying k_3 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_3 studied. The values of k_3 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

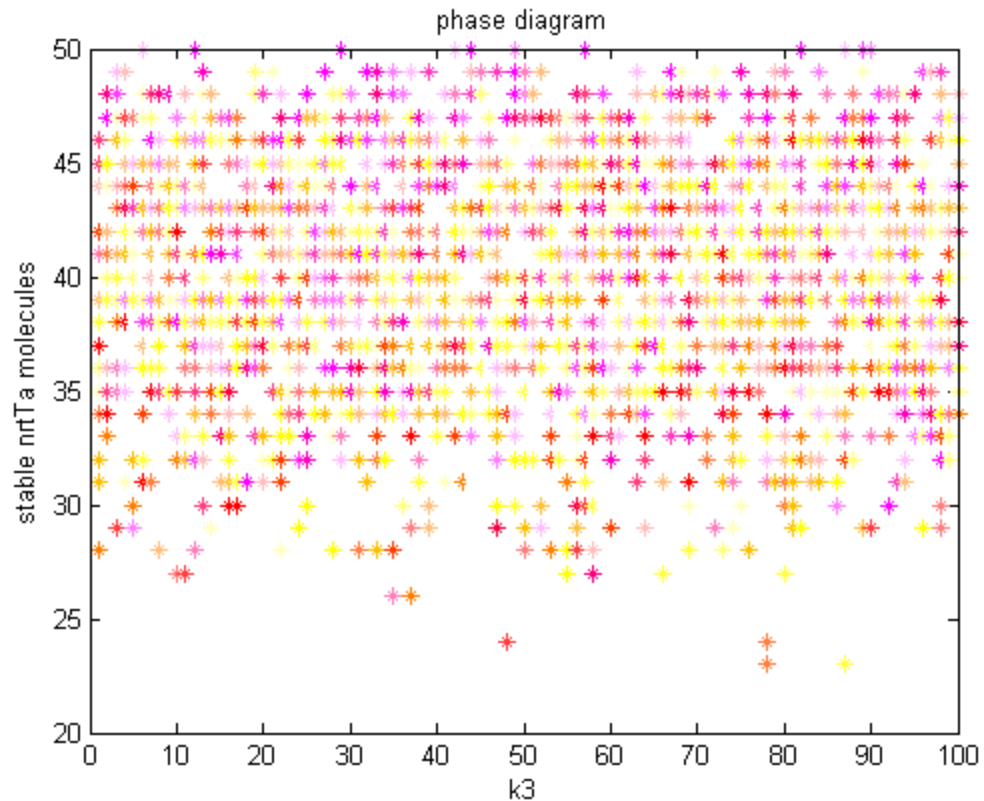


Figure 10. Results of a Bifurcation analysis of the Translation Rate constant(k_3) of the GEV and rtTa mRNA. Plot shows the effect varying k_3 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_3 studied. The values of k_3 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

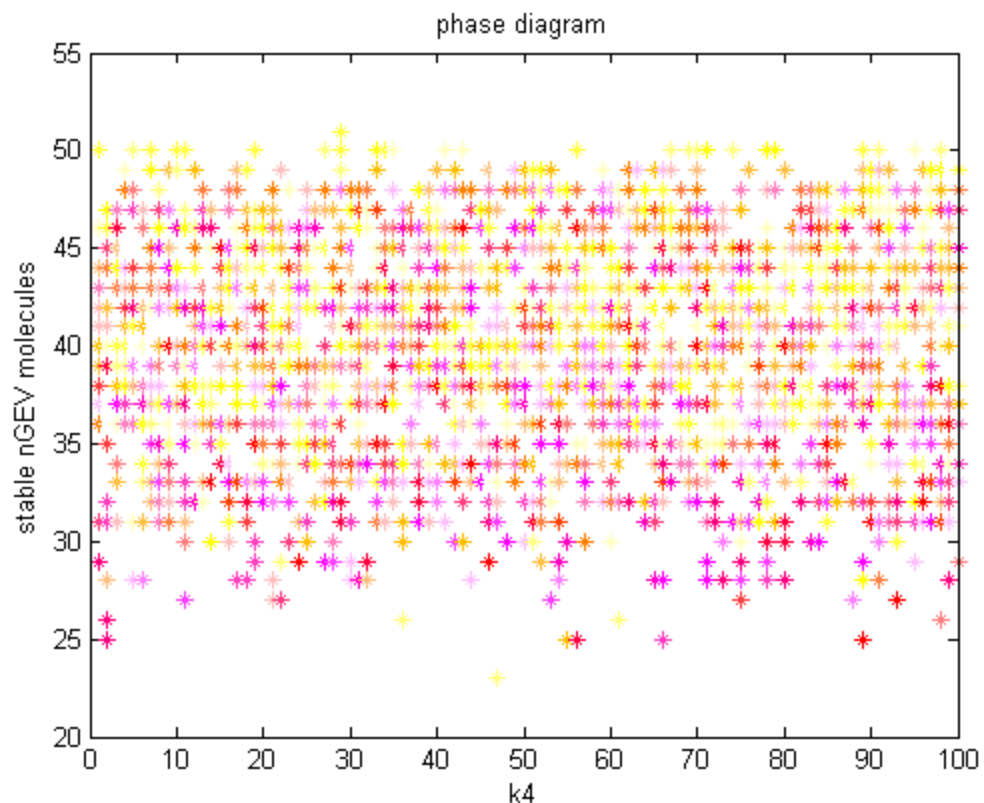


Figure 11. Results of a Bifurcation analysis of the Import Rate constant(k_4) of GEV and rT α from the cytosol to the nucleus. Plot shows the effect varying k_4 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_4 studied. The values of k_4 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

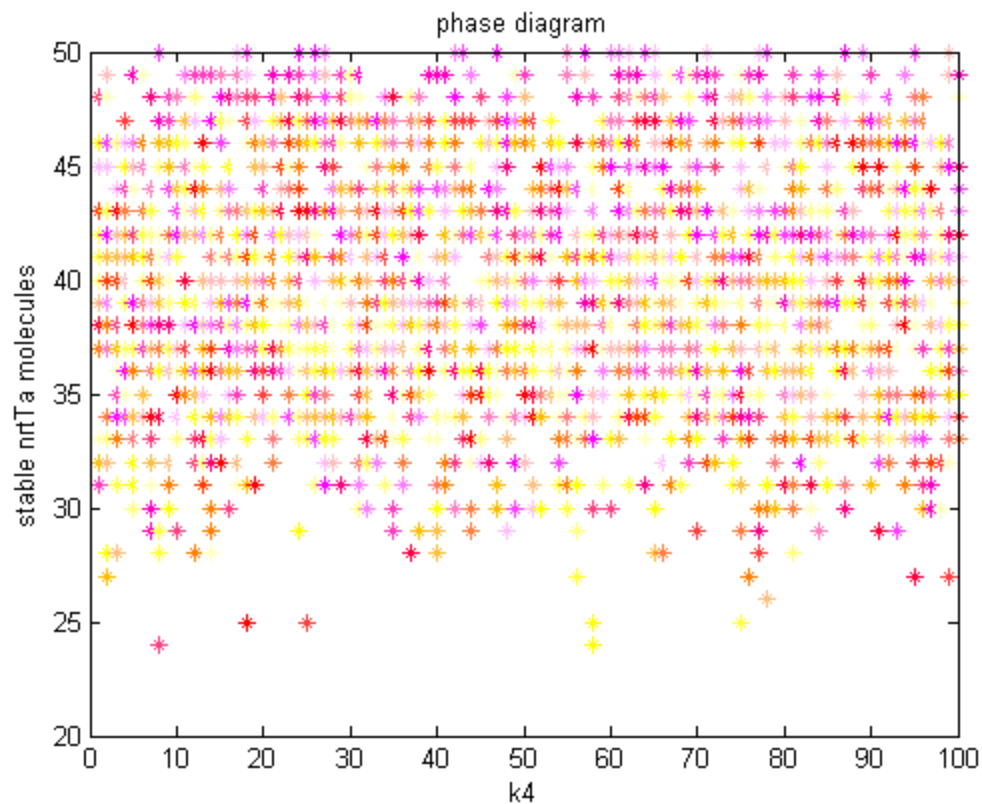


Figure 12. Results of a Bifurcation analysis of the Import Rate constant(k_4) of GEV and rT α from the cytosol to the nucleus. Plot shows the effect varying k_4 has on nrtTa levels. Expression of rT α is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_4 studied. The values of k_4 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

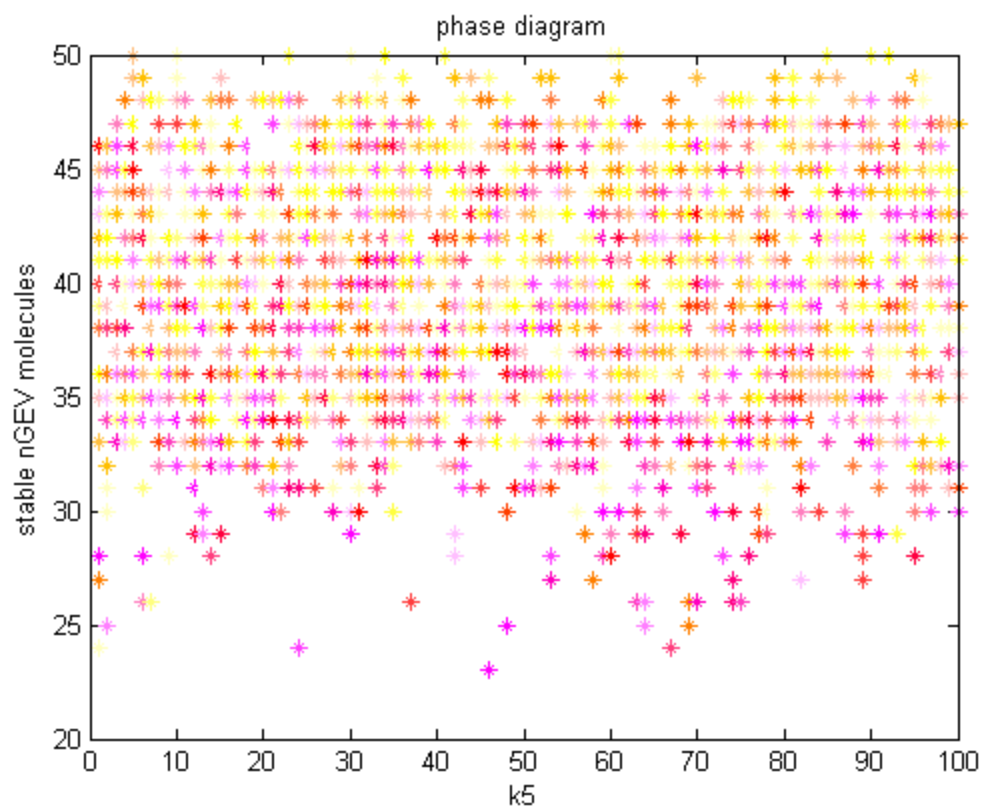


Figure 13. Results of a Bifurcation analysis of the Binding Rate constant(k_5) of GEV and rT α to its inhibitory binding sites. Plot shows the effect varying k_5 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_5 studied. The values of k_5 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

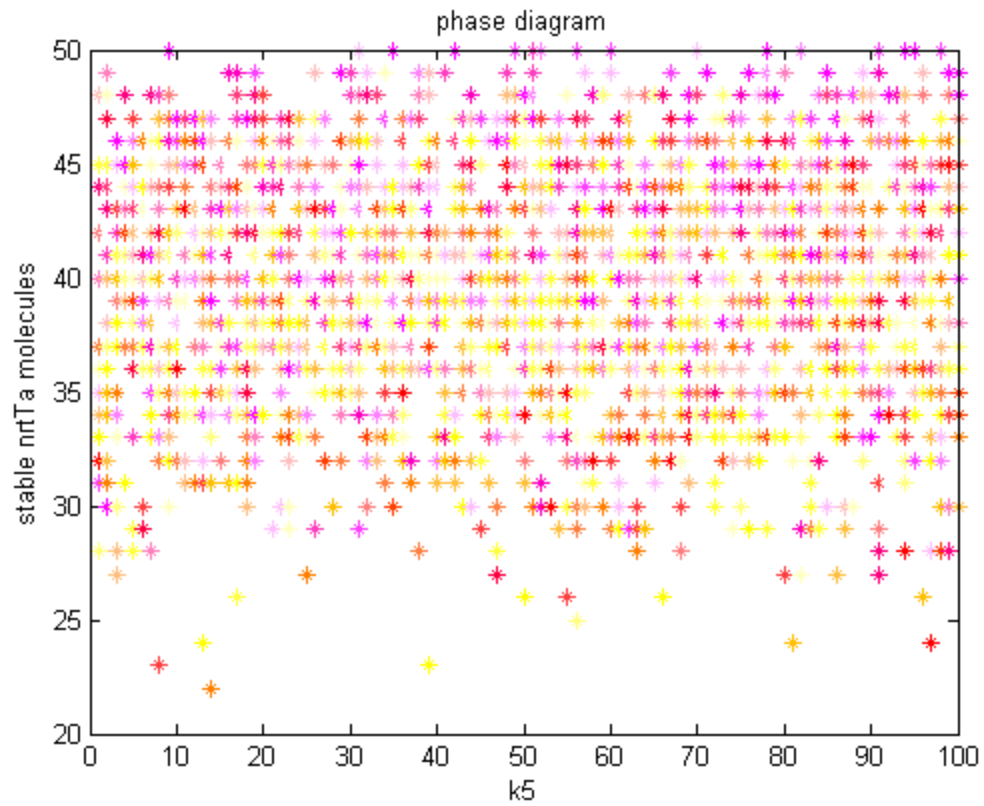


Figure 14. Results of a Bifurcation analysis of the Binding Rate constant(k_5) of GEV and rtTa to its inhibitory binding sites. Plot shows the effect varying k_5 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_5 studied. The values of k_5 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

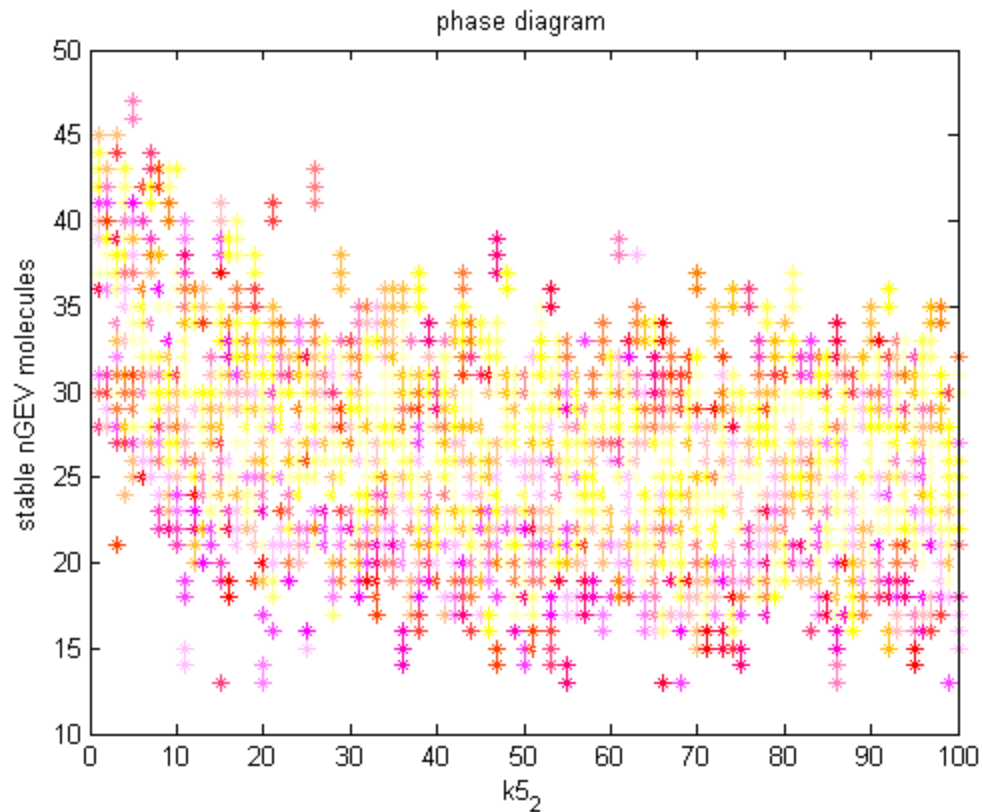


Figure 15. Results of a Bifurcation analysis of the Dissociation Rate constant($k5_2$) of GEV and rtTa from its inhibitory binding sites. Plot shows the effect varying $k5_2$ has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of $k5_2$ studied. The values of $k5_2$ studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

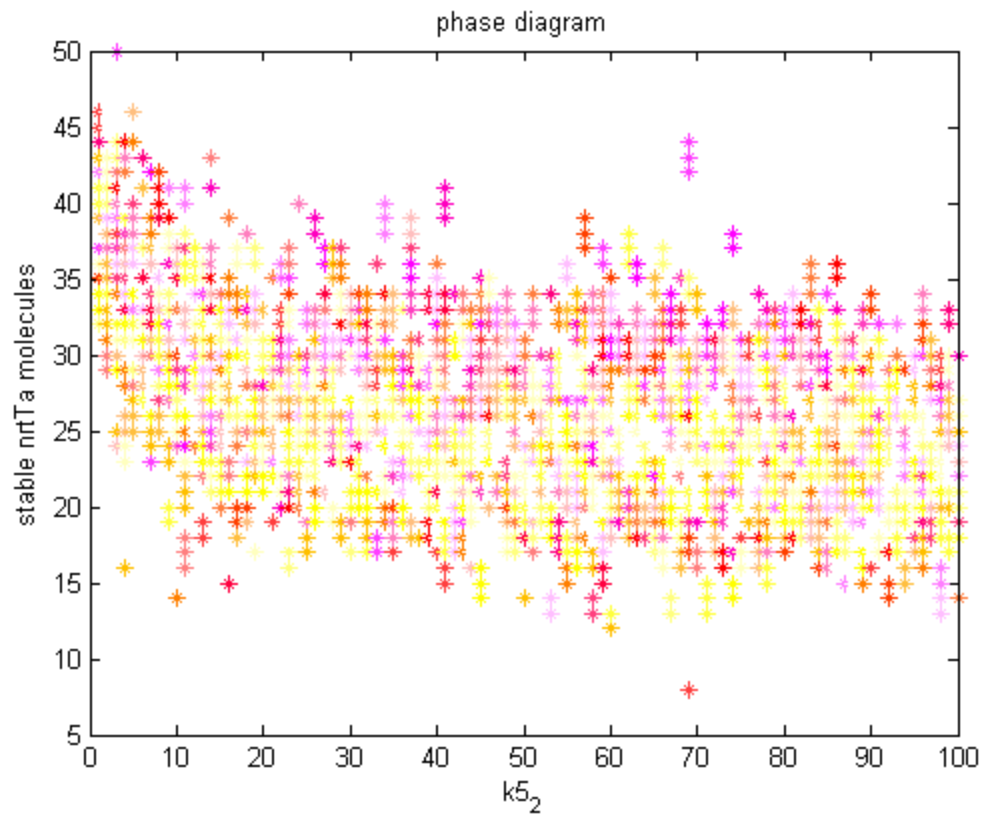


Figure 16. Results of a Bifurcation analysis of the Dissociation Rate constant($k5_2$) of GEV and rtTa from its inhibitory binding sites. Plot shows the effect varying $k5_2$ has on nrtTa levels.

Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of $k5_2$ studied. The values of $k5_2$ studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

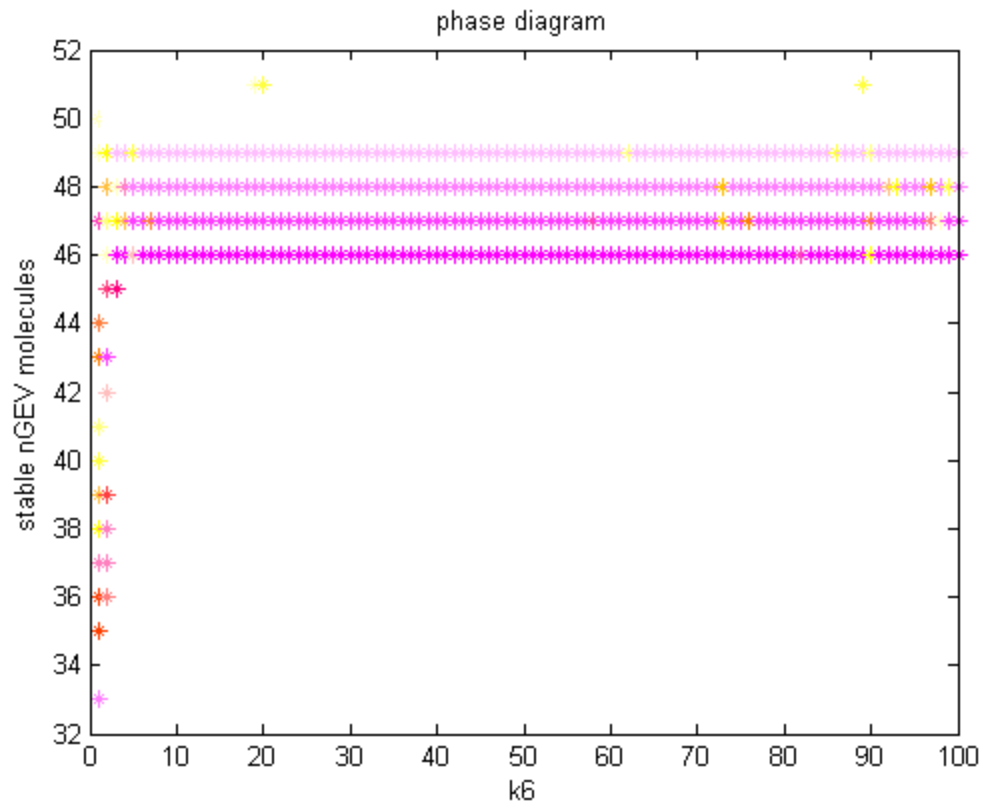


Figure 17. Results of a Bifurcation analysis of the Transcription Rate constant(k_6) of the inhibited GEV and rtTa genes. Plot shows the effect varying k_6 has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_6 studied. The values of k_6 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

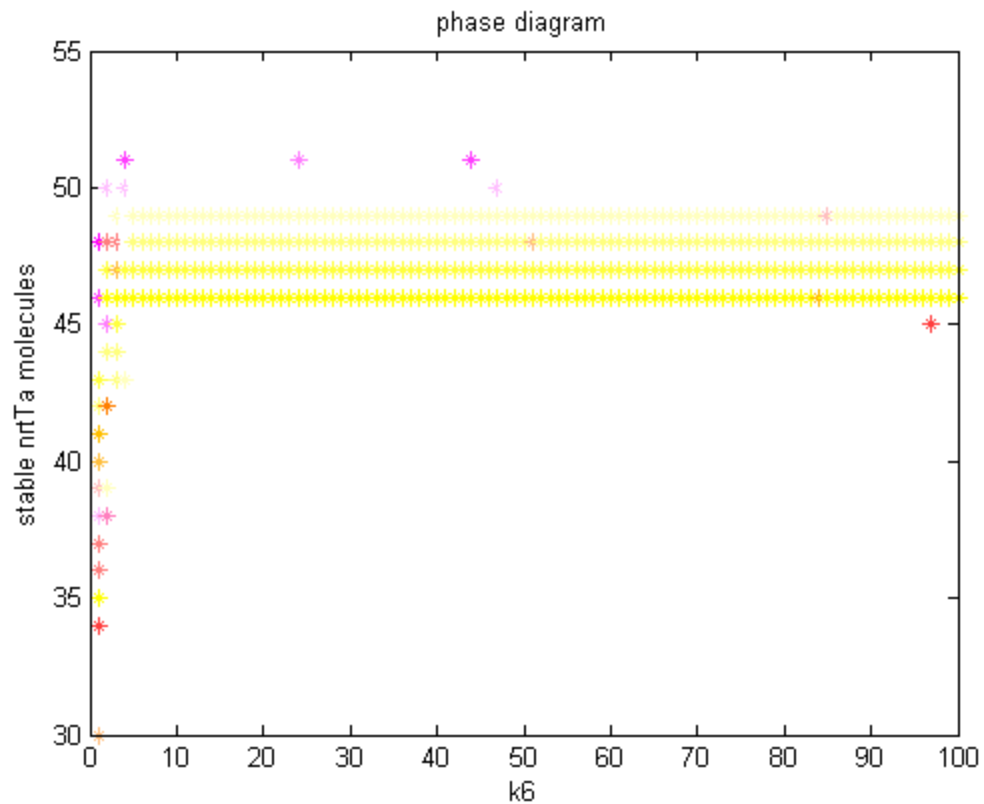


Figure 18. Results of a Bifurcation analysis of the Transcription Rate constant(k_6) of the inhibited GEV and rtTa genes. Plot shows the effect varying k_6 has on nrtTa levels. Expression of rtTa is

measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_6 studied. The values of k_6 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

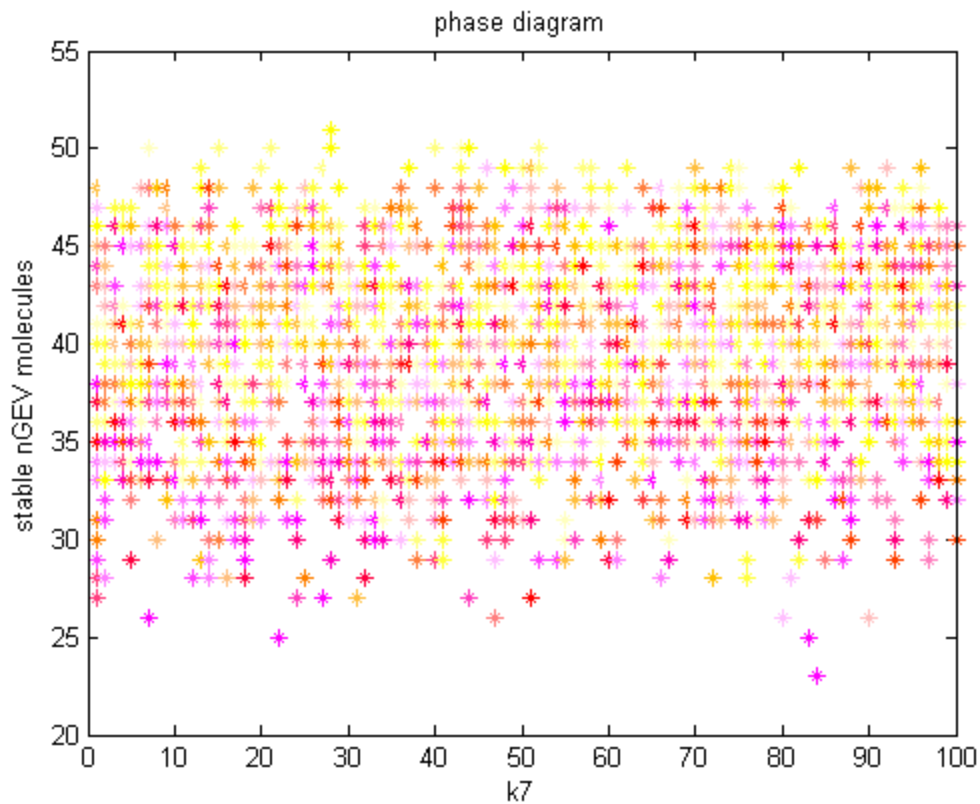


Figure 19. Results of a Bifurcation analysis of the Binding Rate constant(k_7) of GEV and rtTa to its promoter binding sites. Plot shows the effect varying k_7 has on nGEV levels. Expression of

GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_7 studied. The values of k_7 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

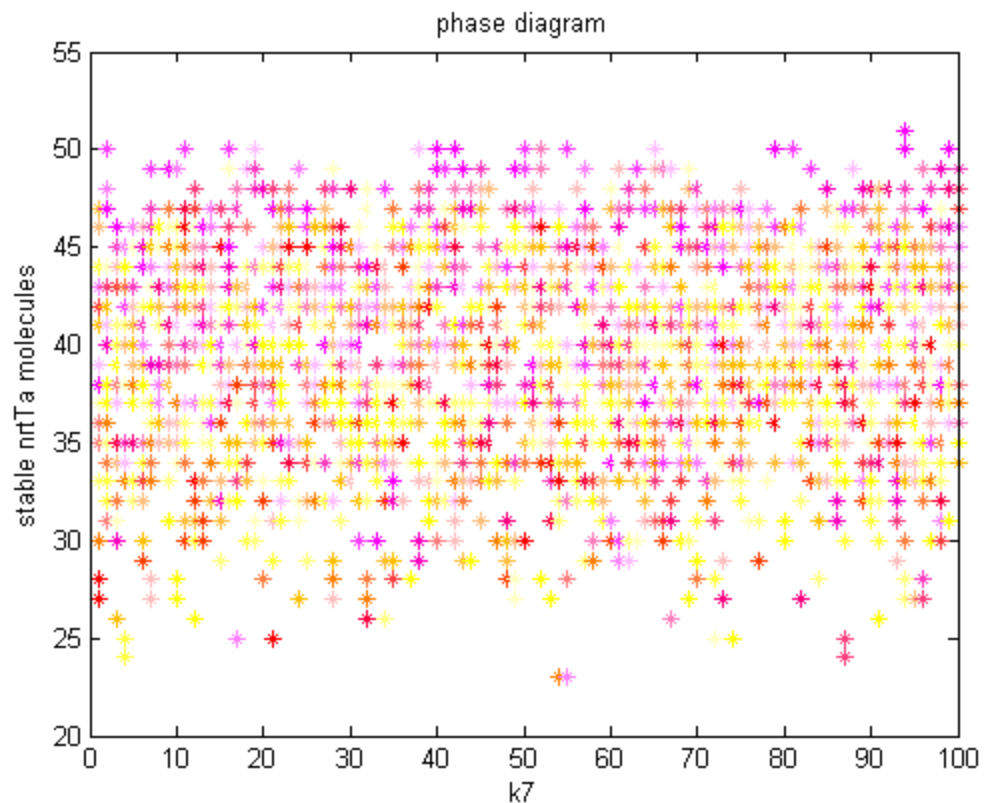


Figure 20. Results of a Bifurcation analysis of the Binding Rate constant(k_7) of GEV and nrtTa to its promoter binding sites. Plot shows the effect varying k_7 has on nrtTa levels. Expression of

rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_7 studied. The values of k_7 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

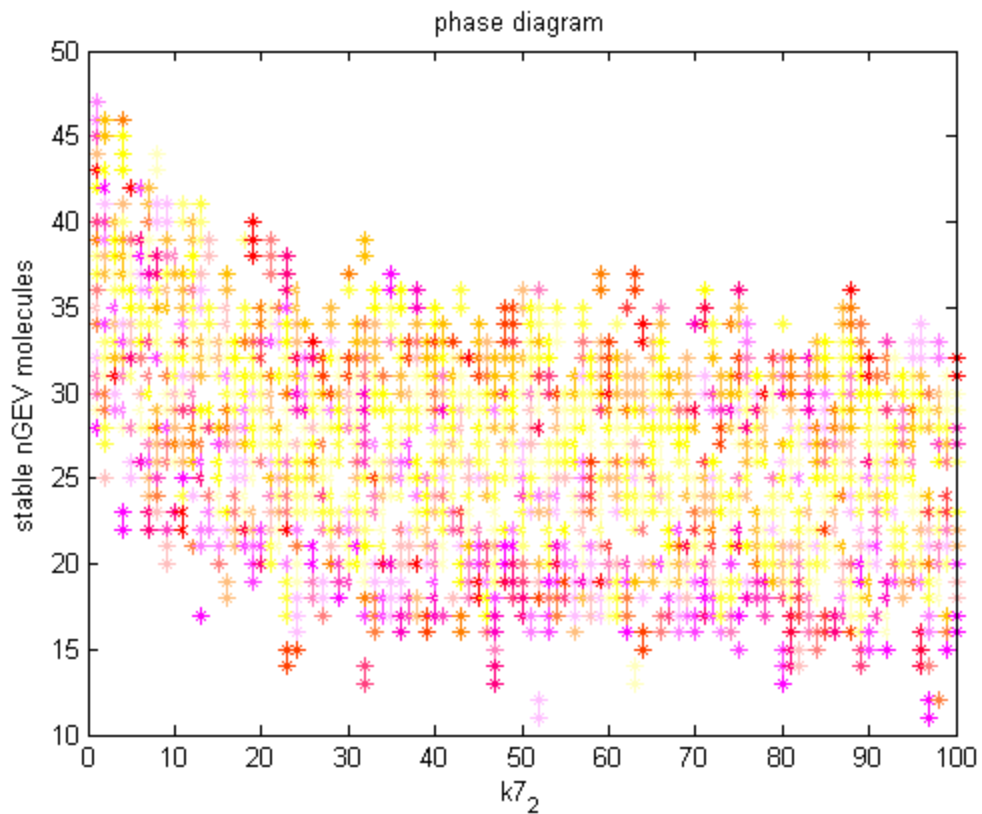


Figure 21. Results of a Bifurcation analysis of the Dissociation Rate constant(k_7) of GEV and rtTa from its promoter binding sites. Plot shows the effect varying k_7 has on nGEV levels.

Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_7 studied. The values of k_7 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

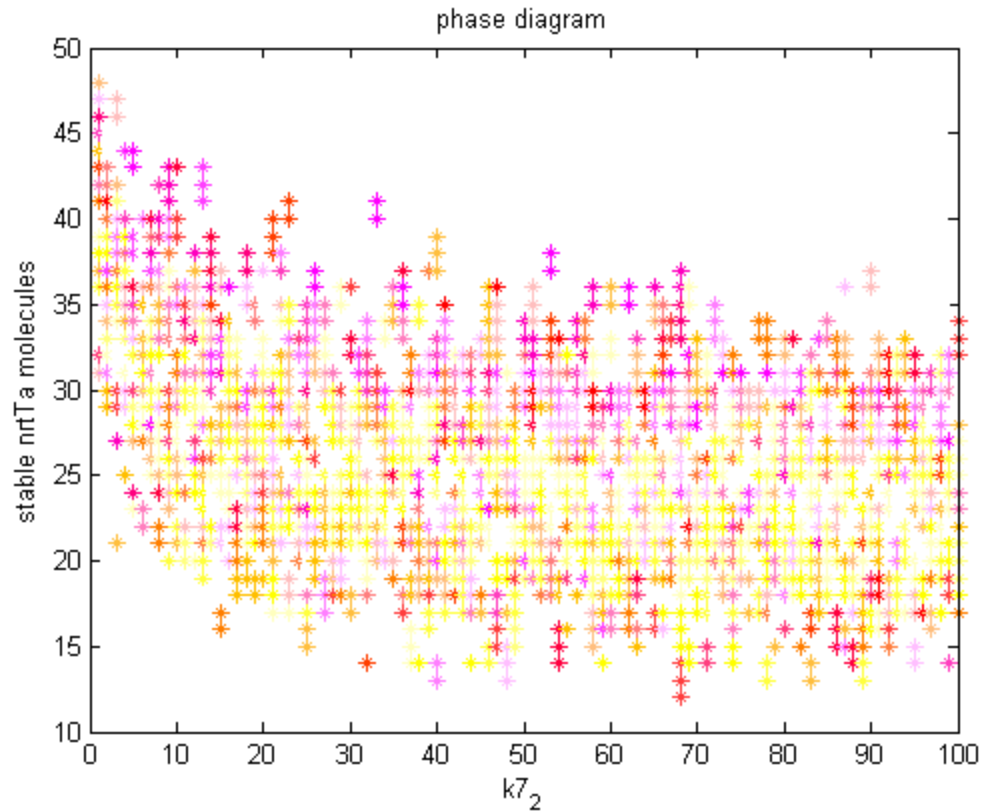


Figure 22. Results of a Bifurcation analysis of the Dissociation Rate constant(k_7) of GEV and rTa from its promoter binding sites. Plot shows the effect varying k_7 has on nrtTa levels. Expression of rTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of

the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_7 studied. The values of k_7 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

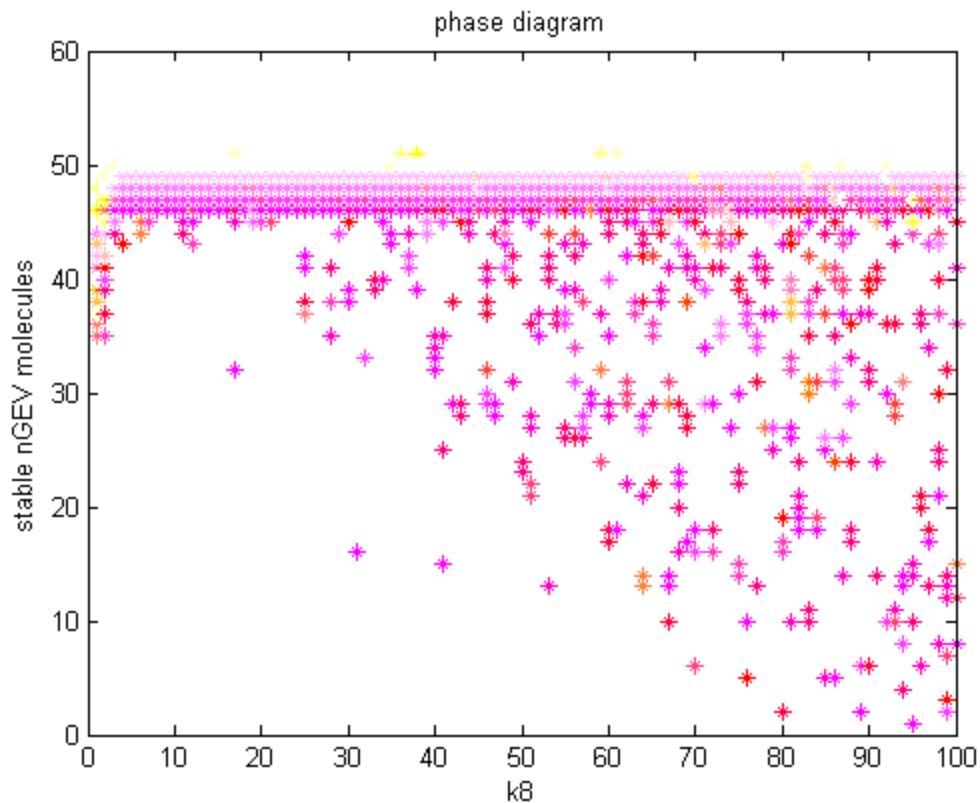


Figure 23. Results of a Bifurcation analysis of the Transcription Rate constant(k_8) of the promoted GEV and rtTa genes. Plot shows the effect varying k_8 has on nGEV levels. Expression

of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_8 studied. The values of k_8 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

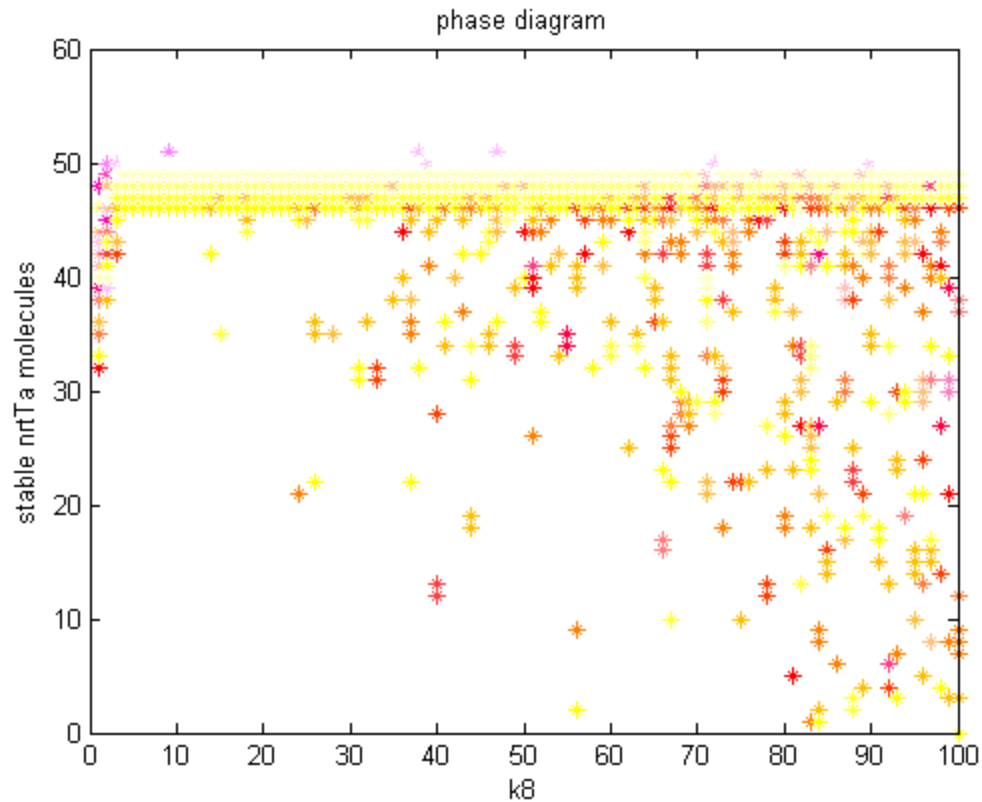


Figure 24. Results of a Bifurcation analysis of the Transcription Rate constant(k_8) of the promoted GEV and rtTa genes. Plot shows the effect varying k_8 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_8 studied. The values of k_8 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

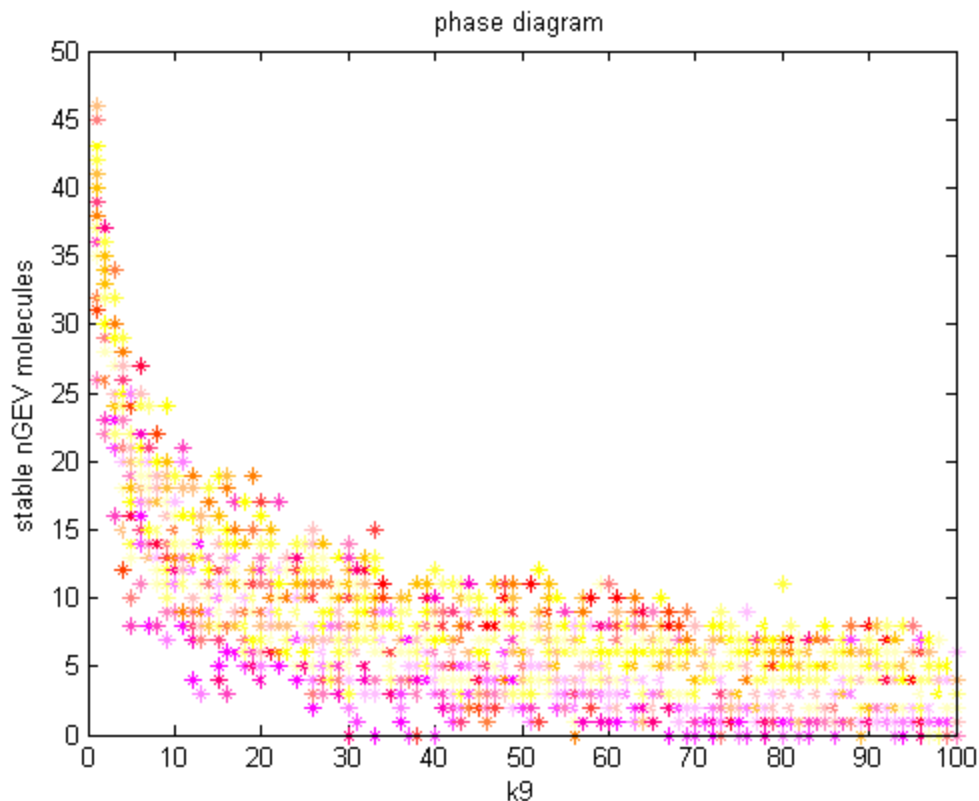


Figure 25. Results of a Bifurcation analysis of the Transcription/Translation Rate constant(k_9) of BFP and GFP. Plot shows the effect varying k_9 has on nGEV levels. Expression of GEV is

measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times (with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_9 studied. The values of k_9 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

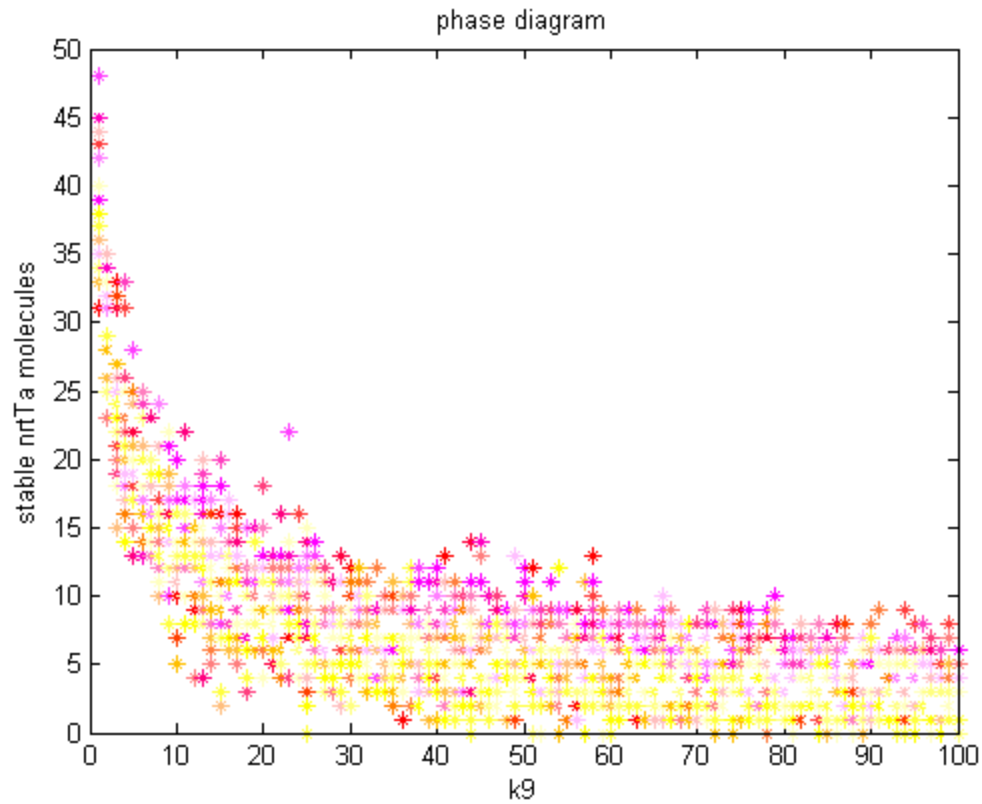


Figure 26. Results of a Bifurcation analysis of the Transcription/Translation Rate constant(k_9) of BFP and GFP. Plot shows the effect varying k_9 has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_9 studied. The values of k_9 studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

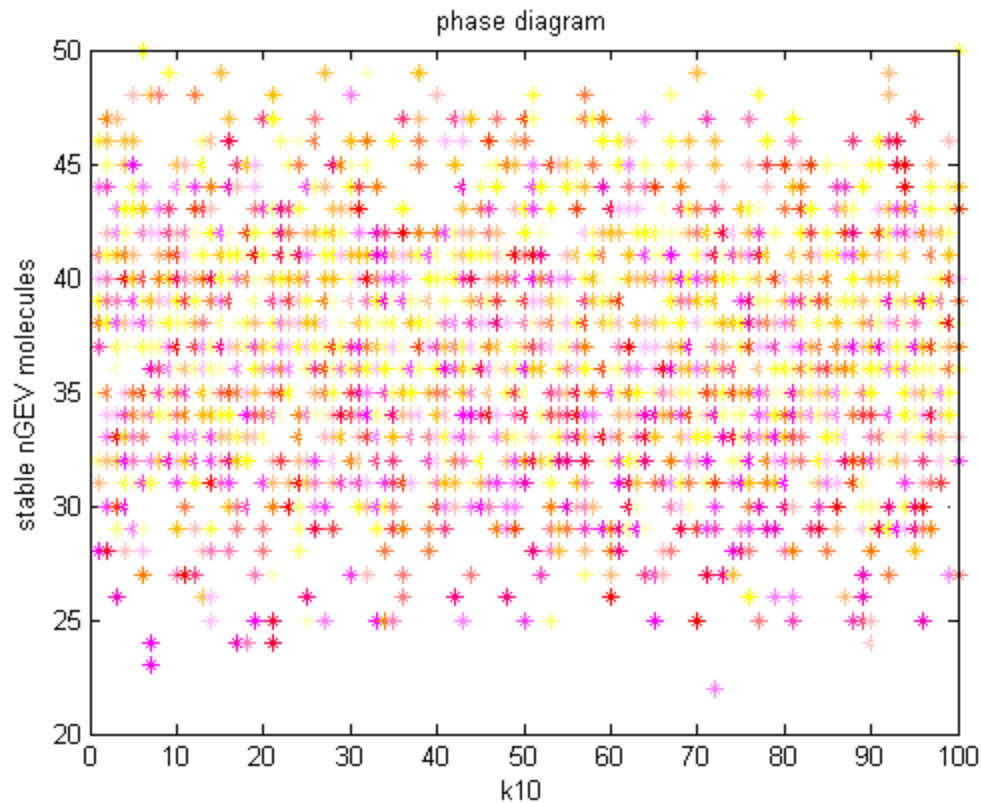


Figure 27. Results of a Bifurcation analysis of the Degradation Rate constant(k_{10}) of BFP and GFP. Plot shows the effect varying k_{10} has on nGEV levels. Expression of GEV is measured by the amount of nGEV found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_{10} studied. The values of k_{10} studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.

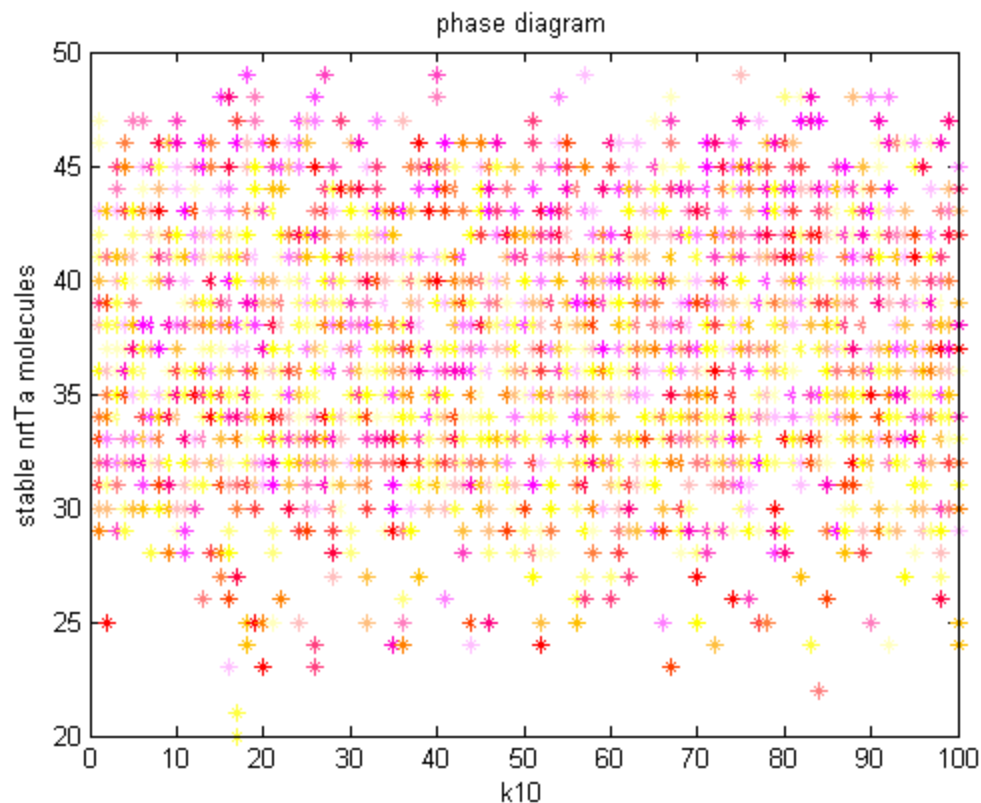


Figure 28. Results of a Bifurcation analysis of the Degradation Rate constant(k_{10}) of BFP and GFP. Plot shows the effect varying k_{10} has on nrtTa levels. Expression of rtTa is measured by the amount of nrtTa found in a cell at the last 5 time-steps of the simulation. The simulation was conducted 25 times(with initial nGEV and nrtTa molecule populations ranging between 0 and 4) for each value of k_{10} studied. The values of k_{10} studied were the 100 integers between 0 and 100. The populations of nGEV at the last 5 time-steps of the simulation are plotted in a different color for every combination of initial nGEV and nrtTa molecule populations. Initial levels of aTc and beta drugs are 50 molecules.